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OM nucleic - nucleic search, using sw model

Run on: November 28, 2002, 17:10:34 : Search time 1444.83 Seconds

(without alignments)
224.186 Million cell updates/sec

Title: US-09-719-737-2

Perfect score: 20

Sequence: 1 gtccacagactgcacact 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

EST:*
1: em_estba:*
2: em_estlum:*
3: em_estlu:*
4: em_estlu:*
5: em_estlu:*
6: em_estlu:*
7: em_estlu:*
8: em_estlu:*
9: em_estlu:*
10: em_estlu:*
11: em_estlu:*
12: em_estlu:*
13: em_estlu:*
14: em_estlu:*
15: em_estlu:*
16: em_estlu:*
17: em_estlu:*
18: em_estlu:*
19: em_estlu:*
20: em_estlu:*
21: em_estlu:*
22: em_estlu:*
23: em_estlu:*
24: em_estlu:*
25: em_estlu:*
26: em_estlu:*
27: em_estlu:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13.6	68.0	36	17	AL752038 Arabidops
2	13.6	68.0	43	17	BH811442 Arabidops
3	12.6	63.0	46	12	BF983620 Arabidops
4	12.4	62.0	40	12	BF784339 Arabidops
5	12.2	61.0	31	17	AZ435998 Arabidops
6	12.2	61.0	40	9	AT708971 Arabidops

7	12.2	61.0	46	9	AA576353 Arabidops
8	12	60.0	50	9	AU103972 Arabidops
9	12	60.0	50	9	AU106874 Arabidops
10	12	60.0	50	9	AU106878 Arabidops
11	11.8	59.0	21	17	AZ647787 Arabidops
12	11.8	59.0	44	14	H44436 Arabidops
13	11.6	58.0	27	17	AZ387826 Arabidops
14	11.6	58.0	39	17	AZ310013 Arabidops
15	11.6	58.0	37	17	AZ338635 Arabidops
16	11.6	58.0	44	17	AZ502054 Arabidops
17	11.6	58.0	45	17	AZ760255 Arabidops
18	11.6	58.0	50	9	AU103964 Arabidops
19	11.6	58.0	50	9	AU103967 Arabidops
20	11.6	58.0	50	9	AU103804 Arabidops
21	11.6	58.0	50	9	AU107143 Arabidops
22	11.6	58.0	50	9	AU107145 Arabidops
23	11.6	58.0	50	9	AU107146 Arabidops
24	11.4	57.0	46	17	AZ768227 Arabidops
25	11.4	57.0	50	9	AU102274 Arabidops
26	11.4	57.0	50	9	AU102275 Arabidops
27	11.2	56.0	27	17	AZ655087 Arabidops
28	11.2	56.0	36	13	BG973952 Arabidops
29	11.2	56.0	37	9	A1647510 Arabidops
30	11.2	56.0	39	13	B1078535 Arabidops
31	11.2	56.0	40	17	AZ378558 Arabidops
32	11.2	56.0	42	14	H14364 Arabidops
33	11.2	56.0	42	17	BH626517 Arabidops
34	11.2	56.0	43	9	AA994992 Arabidops
35	11.2	56.0	43	14	R79446 Arabidops
36	11.2	56.0	44	10	AB844185 Arabidops
37	11.2	56.0	46	12	BF533864 Arabidops
38	11.2	56.0	48	12	BF232745 Arabidops
39	11.2	56.0	48	12	BF235094 Arabidops
40	11.2	56.0	48	17	AZ800533 Arabidops
41	11.2	56.0	49	9	A1560790 Arabidops
42	11.2	56.0	49	9	AA572078 Arabidops
43	11.2	56.0	50	9	AU102678 Arabidops
44	11.2	56.0	50	9	AU104734 Arabidops
45	11.2	56.0	50	9	AU105732 Arabidops

ALIGNMENTS

RESULT 1
LOCUS AL752038/c 36 bp DNA linear GSS 17-JUN-2002
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-010607-014869,
genomic survey sequence.
ACCESSION AL752038
VERSION AL752038.1 GI:21484536
KEYWORDS GSS
SOURCE thale cress
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 Strizhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Saedler,H.,
and Weisshaar,B.
A pipeline for automated high-throughput generation of FSTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
2
Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
A new Arabidopsis thaliana T-DNA mutagenised population (CABI-Kat)
for flanking sequence tag based reverse genetics
UNPUBLISHED
3 (pages 1 to 36)
Rosso,M., Li,Y., Strizhov,N. and Weisshaar,B.
Direct Submission
Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer


```

DEFINITION 60210114F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4238354
ACCESSION 5', mRNA sequence.
VERSION BF784339
KEYWORDS BF784339.1 GI:12089375
SOURCE EST.
ORGANISM house mouse.
            Mus musculus
REFERENCE Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
AUTHORS Mammalia: Eutheria: Rodentia: Sclurognathi: Muridae: Murinae: Mus.
TITLE 1 (bases 1 to 40)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps@email.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1AM949 row: 1 column: 03
High quality sequence stop: 39.
Location/Qualifiers
1. 40
   /organism="Mus musculus"
   /strain="FVB/N"
   /db_xref="taxon:10090"
   /clone="IMAGE:4238354"
   /clone_lib="NCI-CGAP_Kid14"
   /lab_host="DH10B (T1 phage-resistant)"
   /note="Organ: Kidney; Vector: PCMV-SPOrt6; Site:1; Ncti:
   Site:2; Salt: Cloned unidirectionally. Primer: oligo dt.
   Average insert size 1.75 kb. Constructed by Life
   Technologies. Note: this is a NCI-CGAP library. 1"
BASE COUNT 2 a 11 c 17 g 10 t
ORIGIN
Query Match 62.0%; Score 12.4; DB 12; Length 40;
Best Local Similarity 92.9%; Pred. No. 7.1e-04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 6 CAGAGCTTCCACC 19
Db 24 CAGAGCTTCCACC 11

```

```

RESULT 5
A2435998 31 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0222N19F Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION Clone UUC1M0223N19 F. DNA sequence.
ACCESSION A2435998
VERSION A2435998.1 GI:10560011
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
            Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
            Mammalia: Eutheria: Rodentia: Sclurognathi: Muridae: Murinae: Mus.
REFERENCE 1 (bases 1 to 31)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beaconn, T., Duval, B., Hamll, C.,
            Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
            , M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
            and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
            University of Utah
            Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA

```

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FEATURES
source
1. 31
   /organism="Mus musculus"
   /strain="C57BL/6J"
   /db_xref="taxon:10090"
   /clone="UUC1M0223N19"
   /clone_lib="Mouse 10kb plasmid UUC1M library"
   /sex="Male"
   /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
   /note="Vector: pMD42uv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adapted DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pMD42 (g14732114|9b|AF19072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adapted vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
BASE COUNT 5 a 12 c 6 g 8 t
ORIGIN
Query Match 61.0%; Score 12.2; DB 17; Length 31;
Best Local Similarity 82.4%; Pred. No. 8e-04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 4 CCCAGAGCTTGCACCT 20
Db 2 CCCAGAGCTTGCACCT 18

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```

RESULT 6
A1708971 40 bp mRNA linear EST 04-JUN-1999
LOCUS A651d12.X1 Barstead colon HPR4R Homo sapiens cDNA clone
DEFINITION IMAGE:2333207 3' similar to SM.RL10_HUMAN P27635 60S RIBOSOMAL
            PROTEIN L10 ;, mRNA sequence.
ACCESSION A1708971
VERSION A1708971.1 GI:4998747
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
            Mammalia: Eutheria: Primates: Catarrhini: Hominiidae: Homo.
REFERENCE 1 (bases 1 to 40)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Gaisel, G., Jost, S.,
            Krizman, D., Kucuba, T., Lacy, M., Le, N., Lennon, G., Maitra, M., Martin
            , J., Moore, B., Schellenberg, K., Stepien, M., Tan, F., Theising, B.,
            White, Y., Wylie, T., Waterston, R. and Wilson, R.
TITLE WashU-NCI human EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810

```


inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 2 a 4 c 9 g 6 t

Query Match 59.0%; Score 11.8; DB 17; Length 21;
Best Local Similarity 86.7%; Pred. No. 1e+05; 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCCGACGCTTGCCA 17
Db 15 TCCGACGACATGCCA 1

RESULT 12

LOCUS H4436 44 bp mRNA linear EST 31-JUL-1995
DEFINITION yo5b02.s1 Soares breast 3bDbst Homo sapiens cDNA clone
IMAGE:183723 3' similar to gb:M63167 RAC-ALPHA SERINE/THREONINE
KINASE (HUMAN); mRNA sequence.

ACCESSION H4436
VERSION H4436.1 GI:920488
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Hominiidae: Homo. 1 (bases 1 to 44)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston, R., Williamson, A., Woldmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
Insert Size: 643

High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 643 Std Error: 0.00
Seq primer: Promega -21ml3
High quality sequence stop: 1.

FEATURES

SOURCE

1. 44
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:183723"
/clone_1lb="Soares breast 3bDbst"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: breast; Vector: pTT3D (Pharmacia) with a modified polylinker; Site: 1; Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTGCAATCTGACGTGGCGCGCCGCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTT3 vector (Pharmacia). Library went through one round of normalization to a Col - 20. Library constructed by Bento Soares and M.Fatima

BASE COUNT 4 a 15 c 20 g 2 t 3 others

Query Match 59.0%; Score 11.8; DB 14; Length 44;
Best Local Similarity 81.2%; Pred. No. 1.4e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CCCAGCGTTCGCCAC 19
Db 20 CCCAGCGTTCGCCAC 35

RESULT 13

LOCUS A2387826 27 bp DNA linear GSS 02-OCT-2000
DEFINITION HM0147E2R Mouse 10kb plasmid U00C1M library Mus musculus genomic
clone U00C1M0147E22 R, DNA sequence.

ACCESSION A2387826
VERSION A2387826.1 GI:10501534
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus. 1 (bases 1 to 27)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0147 Row: E Column: 22
Seq primer: CACACGAAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.

FEATURES

SOURCE

1. 27
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U00C1M0147E22"
/clone_1lb="Mouse 10kb plasmid U00C1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD24nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (914732114[9b]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells

BASE COUNT 6 a 9 c 3 g 9 t
 ORIGIN

Query Match 58.0%; Score 11.6; DB 17; Length 27;
 Best Local Similarity 77.8%; Pred. No. 1.4e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 TTCCAGAGCTTGCACCC 19
 ||||| 11 11111
 Db 1 TTCCCATAGGCTCCACCC 18

RESULT 14

A2310013 29 bp DNA linear GSS 29-SEP-2000
 LOCUS 1M0018B12R Mouse 10kb plasmid UGCC1M library Mus musculus genomic
 DEFINITION clone UGCC1M0018B12 R, DNA sequence.

ACCESSION A2310013
 VERSION A2310013.1 GI:10351576
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 29)
 AUTHORS Dunn D., Aoyagi A., Barber M., Beacorn T., Duval B., Hamil C., Islam H., Longacre S., Mahmoud M., Meenen E., Pedersen T., Reilly M., Rose M., Rose R., Stokes R., Tinney A., von Niederhausern A. and Wright D., Weis R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 8m. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0018 row: B column: 12
 Seq primer: CACACAGAAACACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 29.
 Location/Qualifiers

FEATURES
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 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCC1M0018B12"
 /clone_lib="Mouse 10kb plasmid UGCC1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1147321149b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells

BASE COUNT 0 a 14 c 6 g 9 t
 ORIGIN

Query Match 58.0%; Score 11.6; DB 17; Length 29;
 Best Local Similarity 77.8%; Pred. No. 1.5e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 TTCCAGAGCTTGCACCT 20
 |||| 1111111 11
 Db 4 TTCCCGTCTGTGCTGCT 21

RESULT 15

A2338635 37 bp DNA linear GSS 29-SEP-2000
 LOCUS 1M006911R Mouse 10kb plasmid UGCC1M library Mus musculus genomic
 DEFINITION clone UGCC1M0069115 R, DNA sequence.

ACCESSION A2338635
 VERSION A2338635.1 GI:10412103
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 37)
 AUTHORS Dunn D., Aoyagi A., Barber M., Beacorn T., Duval B., Hamil C., Islam H., Longacre S., Mahmoud M., Meenen E., Pedersen T., Reilly M., Rose M., Rose R., Stokes R., Tinney A., von Niederhausern A. and Wright D., Weis R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 8m. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0069 row: I column: 15
 Seq primer: CACACAGAAACACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 37.
 Location/Qualifiers

FEATURES
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 1..37
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCC1M0069115"
 /clone_lib="Mouse 10kb plasmid UGCC1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1147321149b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells

BASE COUNT	14 a	11 c	7 g	5 t
ORIGIN	and selected for ampicillin resistance."			

ORIGIN

Query Match

58.08; Score 11.6; DB 17; Length 37;
77.88; Pred NO 1 6e+05.

```

Best Local Similarity 77.88; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 4

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Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTTCCGAGCTGCCAC 18

DB

E

|| | | | | | | | | |

|||||

Db 6 GTCCCTCAAGCTGGCCAC 23

Search completed: November 28, 2002, 19:30:41
Job time : 1447.83 secs

Job time : 1447.83 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 28, 2002, 17:15:39 ; Search time 42.069 Seconds
(without alignments)
183.088 Million cell updates/sec

Title: US-09-719-737-2

Sequence: 1 gtccacagactgccacct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 341543 seqs, 192557720 residues

Total number of hits satisfying chosen parameters: 177872

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published_Applications_NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCY_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 6: /cgn2_6/ptodata/1/pubpna/PCYUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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- 12: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	14.4	72.0	20	10	US-09-752-639-36 Sequence 36, Appl
2	14.4	72.0	20	10	US-09-984-198-36 Sequence 36, Appl
3	13.6	68.0	25	10	US-09-815-153-9 Sequence 9, Appl
4	13.2	66.0	31	10	US-09-801-274-992 Sequence 992, App
5	12.6	63.0	20	10	US-09-841-366A-33 Sequence 33, Appl
6	12.4	62.0	19	10	US-09-216-393-289 Sequence 289, App
7	12.2	61.0	20	9	US-09-944-413-99 Sequence 99, Appl
8	12.2	61.0	20	9	US-09-944-403-99 Sequence 99, Appl
9	12.2	61.0	20	9	US-09-944-896-99 Sequence 99, Appl
10	12.2	61.0	20	9	US-09-944-944-99 Sequence 99, Appl
11	12.2	61.0	20	10	US-09-866-028-99 Sequence 99, Appl
12	12.2	61.0	20	10	US-09-944-449-99 Sequence 99, Appl
13	12.2	61.0	20	10	US-09-944-457-99 Sequence 99, Appl
14	12.2	61.0	20	10	US-09-945-587-99 Sequence 99, Appl
15	12.2	61.0	20	10	US-09-945-015-99 Sequence 99, Appl
16	12.2	61.0	20	10	US-09-944-396-99 Sequence 99, Appl
17	12.2	61.0	20	10	US-09-944-097-99 Sequence 99, Appl
18	12.2	61.0	20	10	US-09-944-432-99 Sequence 99, Appl
19	12.2	61.0	20	10	US-09-943-762-99 Sequence 99, Appl

C 20	12.2	61.0	20	10	US-09-944-654-99	Sequence 99, Appl
C 21	12.2	61.0	20	10	US-09-843-851A-99	Sequence 99, Appl
C 22	12.2	61.0	28	10	US-09-833-381-11	Sequence 11, Appl
C 23	12.2	61.0	26	9	US-09-089-818B-5	Sequence 5, Appl1
C 24	11.8	59.0	20	10	US-09-454-394-61	Sequence 61, Appl1
C 25	11.8	59.0	20	10	US-09-454-394-64	Sequence 64, Appl1
C 26	11.8	59.0	20	10	US-09-791-406-75	Sequence 75, Appl1
C 27	11.8	59.0	35	10	US-09-867-569-5	Sequence 5, Appl1
C 28	11.8	59.0	49	10	US-09-781-907-28	Sequence 28, Appl
C 29	11.6	58.0	34	9	US-09-764-868-1247	Sequence 1247, Appl
C 30	11.4	57.0	16	10	US-09-781-902-52	Sequence 52, Appl1
C 31	11.4	57.0	31	10	US-09-801-274-352	Sequence 352, Appl1
C 32	11.4	57.0	36	9	US-10-127-391-27	Sequence 27, Appl1
C 33	11.4	57.0	39	9	US-09-252-150-59	Sequence 59, Appl1
C 34	11.4	57.0	46	10	US-09-320-337-38	Sequence 38, Appl1
C 35	11.2	56.0	20	10	US-09-733-294A-38	Sequence 38, Appl1
C 36	11.2	56.0	20	10	US-09-733-294A-39	Sequence 39, Appl1
C 37	11.2	56.0	25	9	US-09-978-697-376	Sequence 376, Appl
C 38	11.2	56.0	25	9	US-09-844-684-8	Sequence 376, Appl
C 39	11.2	56.0	30	10	US-09-733-294A-65	Sequence 8, Appl1
C 40	11.1	55.0	22	10	US-09-755-665-68	Sequence 65, Appl1
C 41	11.1	55.0	25	10	US-09-866-108-3303	Sequence 68, Appl1
C 42	11.1	55.0	25	10	US-09-866-108-3304	Sequence 3303, Ap
C 43	11.1	55.0	25	10	US-09-866-108-3305	Sequence 3304, Ap
C 44	11.1	55.0	25	10	US-09-866-108-3306	Sequence 3305, Ap
C 45	11.1	55.0	25	10	US-09-866-108-3306	Sequence 3306, Ap

ALIGNMENTS

RESULT 1

US-09-752-639-36 Application US/09752639

Sequence 36, Application US/09752639

Patent No. US20020091243A1

GENERAL INFORMATION:

APPLICANT: Gatanaga, T.

APPLICANT: Granger, G.A.

TITLE OF INVENTION: Factors Altering Tumor Necrosis

TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods

TITLE OF INVENTION: of Use Thereof

NUMBER OF SEQUENCES: 154

CORRESPONDENCE ADDRESS:

ADDRESS: MORRISON & FOERSTER

STREET: 755 PAGE MILL ROAD

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/752, 639

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCY/US99/10793

FILING DATE:

APPLICATION NUMBER: 09/081,385

FILING DATE:

APPLICATION NUMBER: 08/964,747

FILING DATE: 05-NOV-1997

APPLICATION NUMBER: 60/030,761

FILING DATE: 06-NOV-1996

ATTORNEY/AGENT INFORMATION:

NAME: Wu, Frank

REGISTRATION NUMBER: 41,386

REFERENCE/DOCKET NUMBER: 22000-20577.21

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-813-5600

TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Linear
US-09-752-639-36

Query Match 72.0%; Score 14.4; DB 10; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTTCCAGAGCTTCC 16
DB 1 GTTCCAGAGCTTCC 16

RESULT 2

US-09-984-198-36
Sequence 36, Application US/09984198
Patent No. US20020106679A1
GENERAL INFORMATION:
APPLICANT: Gatanaga, T.
TITLE OF INVENTION: Factors Altering Tumor Necrosis
TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,198
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/10793
FILING DATE:
APPLICATION NUMBER: 09/081,385
FILING DATE:
APPLICATION NUMBER: 09/964,747
FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 60/030,761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wu, Frank
REGISTRATION NUMBER: 41,386
REFERENCE/DOCKET NUMBER: 22000-20577.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Linear
US-09-984-198-36

Query Match 72.0%; Score 14.4; DB 10; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.8e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 GTTCCAGAGCTTCC 16
DB 1 GTTCCAGAGCTTCC 16

RESULT 3

US-09-815-153-9
Sequence 9, Application US/09815153
Patent No. US20020132978A1
GENERAL INFORMATION:
APPLICANT: RASTBELL, LUCA R.
TITLE OF INVENTION: VEGF-MODULATED GENES AND METHODS EMPLOYING THEM
FILE REFERENCE: 10716/34
CURRENT APPLICATION NUMBER: US/09/815,153
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,201
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-815-153-9

Query Match 68.0%; Score 13.6; DB 10; Length 25;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GTTCCAGAGCTTCCACT 20
DB 4 GTTCCAGAGCTTCCGCGCT 23

RESULT 4

US-09-801-274-992
Sequence 992, Application US/09801274
Patent No. US20020032319A1
GENERAL INFORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 2825, 2009-001
CURRENT APPLICATION NUMBER: US/09/801,274
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 60/187,510
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 60/206,129
PRIOR FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 1802
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 992
LENGTH: 31
TYPE: DNA
ORGANISM: Homo sapiens
US-09-801-274-992

Query Match 66.0%; Score 13.2; DB 10; Length 31;
Best Local Similarity 75.0%; Pred. No. 7.6e+02;
Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 GTTCCAGAGCTTCCACT 20
DB 10 GTTCCAGAGCTTCCACT 29

RESULT 5

US-09-841-366A-33
Sequence 33, Application US/09841366A
Patent No. US20020058265A1
GENERAL INFORMATION:
APPLICANT: Bachner, Jeffery W.
APPLICANT: Flanagan, Laura
TITLE OF INVENTION: DETECTION OF MICROSATELLITE INSTABILITY AND ITS USE IN
FILE REFERENCE: 16026-9267
CURRENT APPLICATION NUMBER: US/09/841,366A
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/663,020
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 33
LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: D9S2169 primer
US-09-841-366A-33

Query Match 63.0%; Score 12.6; DB 10; Length 20;
Best Local Similarity 78.9%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 TTCCGACAGCTTGCACCT 20
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DB 1 TTCCCAAAAGTTGCCATCT 19

RESULT 6
US-09-216-393-289
Sequence 289, Application US/09216393
Patent No. US20010014447A1
GENERAL INFORMATION:
APPLICANT: Milhausen, Michael James
TITLE OF INVENTION: TOXOPLASMA GONDI PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: TX-1-C2
CURRENT APPLICATION NUMBER: US/09/216,393
CURRENT FILING DATE: 1998-12-18
EARLIER APPLICATION NUMBER: 08/994,825
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 364
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 289
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-216-393-289

Query Match 62.0%; Score 12.4; DB 10; Length 19;
Best Local Similarity 92.9%; Pred. No. 1.8e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 TTCCGACAGCTTGC 15
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DB 2 TTCCGACAGCTTGC 15

RESULT 7
US-09-944-413-99/c
Sequence 99, Application US/09944413
Patent No. US20020156004A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David

APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gertlisen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavits, Ivar
APPLICANT: Neper, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,413
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: NO. US20020156004A1eember 30, 1999

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: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: No. US20020156041a1ember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28301
: PRIOR FILING DATE: December 1, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: December 16, 1999
: PRIOR APPLICATION NUMBER: PCT/US00/03565
: PRIOR FILING DATE: February 11, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: February 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/05841
: PRIOR FILING DATE: March 2, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/08439
: PRIOR FILING DATE: March 30, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/14042
: PRIOR FILING DATE: May 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/20710
: PRIOR FILING DATE: July 28, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/32678
: PRIOR FILING DATE: December 1, 2000
: PRIOR APPLICATION NUMBER: PCT/US01/06520
: PRIOR FILING DATE: February 28, 2001
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO 99
: LENGTH: 20
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-413-99
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Query Match          61.0%  Score 12.2; DB 9; Length 20;
Best Local Similarity 82.4%  Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 GTTCCGACAGCTTCCCA 17
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DB 17 GTTCCGACCTCTTCCCA 1
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RESULT 8
US-09-944-403-99/c
: Sequence 99: Application US/09944403
: Patent No. US20020165143A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gertlisen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kijavlin, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P2548P1C1
: CURRENT APPLICATION NUMBER: US/09/944,403
: PRIOR FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: 09/866,028
: PRIOR FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: 60/067,411
: PRIOR FILING DATE: December 3, 1997
: PRIOR APPLICATION NUMBER: 60/069,334
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069335
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: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,278
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,425
: PRIOR FILING DATE: December 12, 1997
: PRIOR APPLICATION NUMBER: 60/069,696
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,694
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,702
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,870
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/069,873
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/068,017
: PRIOR FILING DATE: December 18, 1997
: PRIOR APPLICATION NUMBER: 60/070,440
: PRIOR FILING DATE: January 5, 1998
: PRIOR APPLICATION NUMBER: 60/074,086
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/074,092
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/075,945
: PRIOR FILING DATE: February 25, 1998
: PRIOR APPLICATION NUMBER: 60/112,850
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 60/113,296
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 60/146,222
: PRIOR FILING DATE: July 28, 1999
: PRIOR APPLICATION NUMBER: PCT/US98/19330
: PRIOR FILING DATE: September 16, 1998
: PRIOR APPLICATION NUMBER: PCT/US98/25108
: PRIOR FILING DATE: December 1, 1998
: PRIOR APPLICATION NUMBER: 09/216,021
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 09/218,517
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 09/254,311
: PRIOR FILING DATE: March 3, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/12252
: PRIOR FILING DATE: June 22, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: September 15, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28409
: PRIOR FILING DATE: No. US20020165143A1a1ember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: No. US20020165143A1a1ember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28301
: PRIOR FILING DATE: December 1, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: December 16, 1999
: PRIOR APPLICATION NUMBER: PCT/US00/03565
: PRIOR FILING DATE: February 11, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: February 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/05841
: PRIOR FILING DATE: March 2, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/08439
: PRIOR FILING DATE: March 30, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/14042
: PRIOR FILING DATE: May 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/20710
: PRIOR FILING DATE: July 28, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/32678
: PRIOR FILING DATE: December 1, 2000
: PRIOR APPLICATION NUMBER: PCT/US01/06520
: PRIOR FILING DATE: February 28, 2001
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO 99
: LENGTH: 20
: TYPE: DNA
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: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-403-99

Query Match      61.0%   Score 12.2; DB 9;   Length 20;
Best Local Similarity 82.4%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      1 GTTCCGAGAGCTTGCCA 17
        |||||  |||||
Db      17 GTTCCATTCCTTGCCA 1

RESULT 9
US-09-944-896-99/c
: Sequence 99, Application US/09944896
: Patent No. US20020168715A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gottfredsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gunney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kijavits, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P2548P1C1
: CURRENT APPLICATION NUMBER: US/09/944,896
: PRIOR FILING DATE: 2001-08-31
: PRIOR APPLICATION NUMBER: 09/866,028
: PRIOR FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: 60/069,334
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069335
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,278
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,425
: PRIOR FILING DATE: December 12, 1997
: PRIOR APPLICATION NUMBER: 60/069,696
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,694
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,702
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,870
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/069,873
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/068,017
: PRIOR FILING DATE: December 18, 1997
: PRIOR APPLICATION NUMBER: 60/070,440
: PRIOR FILING DATE: January 5, 1998
: PRIOR APPLICATION NUMBER: 60/074,086
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/074,092
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/075,945
: PRIOR FILING DATE: February 25, 1998
: PRIOR APPLICATION NUMBER: 60/112,850
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 60/113,296
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: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 60/146,222
: PRIOR FILING DATE: July 28, 1999
: PRIOR APPLICATION NUMBER: PCT/US98/19330
: PRIOR FILING DATE: September 16, 1998
: PRIOR APPLICATION NUMBER: PCT/US98/25108
: PRIOR FILING DATE: December 1, 1998
: PRIOR APPLICATION NUMBER: 09/216,021
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 09/218,517
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 09/254,311
: PRIOR FILING DATE: March 3, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/12252
: PRIOR FILING DATE: June 22, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: September 15, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28409
: PRIOR FILING DATE: No. US20020168715A1 December 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: No. US20020168715A1 December 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28301
: PRIOR FILING DATE: December 1, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: December 16, 1999
: PRIOR APPLICATION NUMBER: PCT/US00/03565
: PRIOR FILING DATE: February 11, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: February 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/05841
: PRIOR FILING DATE: March 2, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/08439
: PRIOR FILING DATE: March 30, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/14042
: PRIOR FILING DATE: May 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/20710
: PRIOR FILING DATE: July 28, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/32678
: PRIOR FILING DATE: December 1, 2000
: PRIOR APPLICATION NUMBER: PCT/US01/06520
: PRIOR FILING DATE: February 28, 2001
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO 99
: LENGTH: 20
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-896-99

Query Match      61.0%   Score 12.2; DB 9;   Length 20;
Best Local Similarity 82.4%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      1 GTTCCGAGAGCTTGCCA 17
        |||||  |||||
Db      17 GTTCCATTCCTTGCCA 1

RESULT 10
US-09-944-99/c
: Sequence 99, Application US/09944944
: Patent No. US20020173463A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gottfredsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
```

APPLICANT: Gurney,Austin
 APPLICANT: Hillan,Kenneth
 APPLICANT: Kijavini,Ivar
 APPLICANT: Napier,Mary
 APPLICANT: Roy,Margaret
 APPLICANT: Tumas,Daniel
 APPLICANT: Wood,William
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P254BP1C1
 CURRENT APPLICATION NUMBER: US/09/944,944
 PRIOR FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: 09/866,028
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/067,411
 PRIOR FILING DATE: December 3, 1997
 PRIOR APPLICATION NUMBER: 60/069,334
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,335
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,278
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,425
 PRIOR FILING DATE: December 12, 1997
 PRIOR APPLICATION NUMBER: 60/069,696
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,694
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,702
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,870
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/069,873
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/068,017
 PRIOR FILING DATE: December 18, 1997
 PRIOR APPLICATION NUMBER: 60/070,440
 PRIOR FILING DATE: January 5, 1998
 PRIOR APPLICATION NUMBER: 60/074,086
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/074,092
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/075,945
 PRIOR FILING DATE: February 23, 1998
 PRIOR APPLICATION NUMBER: 60/112,850
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 60/113,296
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 60/146,222
 PRIOR FILING DATE: July 28, 1999
 PRIOR APPLICATION NUMBER: PCT/US98/19330
 PRIOR FILING DATE: September 16, 1998
 PRIOR APPLICATION NUMBER: PCT/US98/25108
 PRIOR FILING DATE: December 1, 1998
 PRIOR APPLICATION NUMBER: 09/216,021
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 09/218,517
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 09/254,311
 PRIOR FILING DATE: March 3, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/12252
 PRIOR FILING DATE: June 22, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/21090
 PRIOR FILING DATE: September 15, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28409
 PRIOR FILING DATE: No. US20020173463A1
 PRIOR APPLICATION NUMBER: PCT/US99/28313
 PRIOR FILING DATE: No. US20020173463A1
 PRIOR APPLICATION NUMBER: PCT/US99/28301
 PRIOR FILING DATE: December 1, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/30095
 PRIOR FILING DATE: December 16, 1999
 PRIOR APPLICATION NUMBER: PCT/US00/03565

PRIOR FILING DATE: February 11, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR FILING DATE: February 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/05841
 PRIOR FILING DATE: March 2, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/08439
 PRIOR FILING DATE: March 30, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/14042
 PRIOR FILING DATE: May 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/20710
 PRIOR FILING DATE: July 28, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/32678
 PRIOR FILING DATE: December 1, 2000
 PRIOR APPLICATION NUMBER: PCT/US01/06520
 PRIOR FILING DATE: February 28, 2001
 NUMBER OF SEQ ID NOS: 120
 SEQ ID NO 99
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic oligonucleotide probe
 US-09-944-944-99

Query Match 61.0%; Score 12.2; DB 9; Length 20;
 Best Local Similarity 82.4%; Pred. No. 2.2e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GTCCAGACCTTCCA 17
 DB 17 GTCCATCTCTTCCA 1

RESULT 11
 US-09-866-028-99/c
 Sequence 99, Application US/09866028
 Patent No. US20020058309A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
 APPLICANT: Botstein, David
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Filvarsoff, Ellen
 APPLICANT: Gerritsen, Mary
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul
 APPLICANT: Grimaldi, Christopher
 APPLICANT: Gurney, Austin
 APPLICANT: Hillan, Kenneth
 APPLICANT: Kijavini, Ivar
 APPLICANT: Napier, Mary
 APPLICANT: Roy, Margaret
 APPLICANT: Tumas, Daniel
 APPLICANT: Wood, William
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P254BP1C1
 CURRENT APPLICATION NUMBER: US/09/866,028
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION data removed - consult PALM or file wrapper
 NUMBER OF SEQ ID NOS: 120
 SEQ ID NO 99
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic oligonucleotide probe
 US-09-866-028-99

Query Match 61.0%; Score 12.2; DB 10; Length 20;
 Best Local Similarity 82.4%; Pred. No. 2.2e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTTCCAGAGCTTGCCA 17
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Db 17 GTTCCAGTTCCTTGCCA 1

RESULT 12
US-09-944-449-99/c
Sequence 99, Application US/09944449
Patent No. US20020102647A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavich, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,449
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 23, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,256
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998

PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020102647A1 December 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020102647A1 December 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 99
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-449-99

Query Match 61.0%; Score 12.2; DB 10; Length 20;
Best Local Similarity 82.4%; Pred. No. 2, 2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTTCCAGAGCTTGCCA 17
||||| |||||
Db 17 GTTCCAGTTCCTTGCCA 1

RESULT 13
US-09-944-457-99/c
Sequence 99, Application US/09944457
Patent No. US20020110859A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavich, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US/09/944,457
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12232
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020110859A1cember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020110859A1cember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000

PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 99
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide probe
us-09-944-457-99
Query Match 61.0%; Score 12.2; DB 10; Length 20;
Best Local Similarity 82.4%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GTTCCAGAGCTTGCA 17
DB 17 GTTCCAGCTTGCA 1
RESULT 14
US-09-945-587-99/c
Sequence 99, Application US/09945587
Patent No. US20020127643A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Geriltsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillen, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US/09/945,587
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873

;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/068,017
;; PRIOR FILING DATE: December 18, 1997
;; PRIOR APPLICATION NUMBER: 60/070,440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074,086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074,092
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/075,945
;; PRIOR FILING DATE: February 25, 1998
;; PRIOR APPLICATION NUMBER: 60/112,850
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 60/113,296
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/146,222
;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1998
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020127643A,ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US20020127643A,ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 99
;; LENGTH: 20
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-945-587-99

Query Match 61.0%; Score 12.2; DB 10; Length 20;
Best Local Similarity 82.4%; Pred.No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GTTCCGAGACTTGCCA 17
DB 17 GTTCCGACTTGCCA 1

RESULT 15
US-09-945-015-99/c
;; Sequence 99, Application US/09945015
;; Patent No. US20020132768A1
;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin
;; APPLICANT: Bolstein, David
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Gerritsen, Mary
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul
;; APPLICANT: Grimaldi, Christopher
;; APPLICANT: Gurney, Austin
;; APPLICANT: Hillan, Kenneth
;; APPLICANT: Kljavin, Iyar
;; APPLICANT: Napier, Mary
;; APPLICANT: Roy, Margaret
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Wood, William
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P2548P1C1
;; CURRENT APPLICATION NUMBER: US/09/945,015
;; CURRENT FILING DATE: 2001-09-26
;; PRIOR APPLICATION NUMBER: 09/866,028
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/067,411
;; PRIOR FILING DATE: December 3, 1997
;; PRIOR APPLICATION NUMBER: 60/069,334
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069335
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,278
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,425
;; PRIOR FILING DATE: December 12, 1997
;; PRIOR APPLICATION NUMBER: 60/069,696
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,694
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,702
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,870
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/069,873
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/068,017
;; PRIOR FILING DATE: December 18, 1997
;; PRIOR APPLICATION NUMBER: 60/070,440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074,086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074,092
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/075,945
;; PRIOR FILING DATE: February 25, 1998
;; PRIOR APPLICATION NUMBER: 60/112,850
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 60/113,296
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/146,222
;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311

;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 99
;; LENGTH: 20
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-945-015-99

Query Match 61.0%; Score 12.2; DB 10; Length 20;
Best Local Similarity 82.4%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

OY 1 GTTCCAGAGCTTGCCA 17
||||||| |||||
DB 17 GTTCCAGCTCTTGCCA 1

Search completed: November 28, 2002, 19:35:04
Job time : 43.069 secs

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OM nucleic - nucleic search, using sw model

Run on: November 28, 2002, 17:12:29 ; Search time 40.3448 Seconds

(without alignments)
152.028 Million cell updates/sec

Title: US-09-719-737-2

Perfect score: 20

Sequence: 1 gtccacagagcttgcacact 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 509818

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCITUS.COMB.seq:*

6: /cgn2_6/ptodata/2/ina/Backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13.4	67.0	17	3	US-08-998-099-89
2	13.4	67.0	20	4	US-09-476-256-5
3	13.4	67.0	20	4	US-09-476-256-11
4	13.4	67.0	20	4	US-09-844-634-158
5	13.2	66.0	45	6	5395760-9
6	13	65.0	35	4	US-09-039-198A-21
7	13	65.0	35	4	US-09-267-574-21
8	12.4	62.0	38	3	US-09-323-082A-40
9	12.4	61.0	18	3	US-09-344-579-22
10	12.2	61.0	19	1	US-08-358-782D-5
11	12.2	61.0	19	1	US-08-764-527A-5
12	12.2	61.0	24	1	US-08-066-325-5
13	12.2	61.0	28	3	US-08-483-316-5
14	12.2	61.0	28	4	US-08-500-306-1
15	12.2	61.0	28	4	US-09-521-668B-7
16	12.2	61.0	28	5	PCT-US85-12624-5
17	12.2	61.0	33	1	US-07-951-715A-59
18	12.2	61.0	33	1	US-08-459-448A-59
19	12.2	61.0	33	3	US-08-459-595A-59
20	12.2	61.0	33	3	US-08-459-504B-59
21	12.2	61.0	33	3	US-08-459-444-59
22	12.2	61.0	33	4	US-09-547-422-59
23	12.2	61.0	35	3	US-08-435-568A-33
24	12.2	61.0	41	3	US-08-483-316-7
25	12.2	61.0	41	5	PCT-US85-12624-7
26	12	60.0	26	1	US-08-887-997B-5
27	12	60.0	27	1	US-08-434-503-41

28	12	60.0	34	4	US-09-432-020B-41	Sequence 41, Appl
29	12	60.0	42	1	US-07-834-539A-13	Sequence 13, Appl
30	12	60.0	42	1	US-08-053-131-21	Sequence 21, Appl
31	12	60.0	42	1	US-08-053-131-65	Sequence 65, Appl
32	12	60.0	42	1	US-08-645-641-21	Sequence 21, Appl
33	12	60.0	42	1	US-08-645-641-65	Sequence 65, Appl
34	12	60.0	42	1	US-07-853-408B-21	Sequence 21, Appl
35	12	60.0	42	1	US-07-853-408B-65	Sequence 65, Appl
36	12	60.0	42	1	US-08-096-762-21	Sequence 21, Appl
37	12	60.0	42	1	US-08-096-762-65	Sequence 65, Appl
38	12	60.0	42	2	US-08-800-353-13	Sequence 13, Appl
39	12	60.0	42	2	US-08-308-865-21	Sequence 21, Appl
40	12	60.0	42	2	US-08-308-865-65	Sequence 65, Appl
41	12	60.0	42	4	US-09-042-353-189	Sequence 189, App
42	12	60.0	42	4	US-09-042-353-226	Sequence 226, App
43	12	60.0	42	4	US-08-758-417A-37	Sequence 37, Appl
44	12	60.0	42	4	US-08-758-417A-74	Sequence 74, Appl
45	12	60.0	42	5	PCT-US92-06185-13	Sequence 13, Appl

ALIGNMENTS

```
RESULT 1
US-08-998-099-89
; Sequence 89, Application US/08998099A
; Patent No. 6103890
; GENERAL INFORMATION:
; APPLICANT: JARVIS, THALE
; APPLICANT: MCSWIGGEN, JAMES A.
; TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT OF DISEASES
; FILE REFERENCE: 231/175
; CURRENT APPLICATION NUMBER: US/08/998,099A
; EARLIER FILING DATE: 1997-12-24
; EARLIER APPLICATION NUMBER: 60/037,658
; EARLIER FILING DATE: 1997-01-23
; EARLIER APPLICATION NUMBER: 08/373,124
; EARLIER FILING DATE: 1995-01-13
; EARLIER APPLICATION NUMBER: 08/245,466
; EARLIER FILING DATE: 1994-05-18
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 89
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-08-998-099-89
Query Match      67.0% Score 13.4; DB 3; Length 17;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy      5 CCAGAGCTTGCACAC 19
Db      1 CCAGAGGUGCCACAC 15
      ||||| :|||||
US-09-476-256-5/C
; Sequence 5, Application US/09476256
; Patent No. 6228592
; GENERAL INFORMATION:
; APPLICANT: Laboratory of Molecular Biophotonics
; TITLE OF INVENTION: Nucleic Acid Detection in Cytoplasm
; FILE REFERENCE: BBP99-02
; CURRENT APPLICATION NUMBER: US/09/476,256
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
```

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: probe
US-09-476-256-5

Query Match 67.0%; Score 13.4; DB 4; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCAGAGCTTGCACC 19
||||| |||||
DB 20 CCAGAGCTTGCACC 6

RESULT 3
US-09-476-256-11/C
Sequence 11, Application US/09476256
Patent No. 6228592
GENERAL INFORMATION:
APPLICANT: Laboratory of Molecular Biophotonics
TITLE OF INVENTION: Nucleic Acid Detection in Cytoplasm
FILE REFERENCE: BHP99-02
CURRENT APPLICATION NUMBER: US/09/476.256
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 11
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: probe
US-09-476-256-11

Query Match 67.0%; Score 13.4; DB 4; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCAGAGCTTGCACC 19
||||| |||||
DB 20 CCAGAGCTTGCACC 6

RESULT 4
US-09-844-634-158/C
Sequence 158, Application US/09844634
Patent No. 6410324
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
TITLE OF INVENTION: ANTISENSE MODULATION OF TUMOR NECROSIS FACTOR RECEPTOR 2 EXPRESSION
FILE REFERENCE: RTS-0216
CURRENT APPLICATION NUMBER: US/09/844.634
CURRENT FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 174
SEQ ID NO 158
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-844-634-158

Query Match 67.0%; Score 13.4; DB 4; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTCGCCAGAGCTTGC 15
|| |||||
DB 15 CTCGCCAGAGCTTGC 1

RESULT 5
5395760-9/C

Patent No. 5395760
APPLICANT: SMITH, CRAIG A.; GOODWIN, RAYMOND G.; BECKMANN, M. PATRICIA
TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-8 AND B-RECEPTORS
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/523.635
FILING DATE: 10-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 421,417
FILING DATE: 13-OCT-1989
APPLICATION NUMBER: 405,370
FILING DATE: 11-SEP-1989
APPLICATION NUMBER: 403,241
FILING DATE: 05-SEP-1989
SEQ ID NO: 9
LENGTH: 45
5395760-9

Query Match 66.0%; Score 13.2; DB 6; Length 45;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTCCAGAGCTTGCACC 19
||||| | |||||
DB 30 TTCCAGAGCTTGCACC 13

RESULT 6
US-09-039-198A-21
Sequence 21, Application US/09039198A
Patent No. 6200951
GENERAL INFORMATION:
APPLICANT: Gray, Patrick W.
TITLE OF INVENTION: Tjoelker, Larry W.
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039.198A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rln-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
US-09-039-198A-21

Query Match 65.0%; Score 13; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;

Matches 13: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TTCCGAGAGCTTG 14
 |||||
 Db 8 TTCCGAGAGCTTG 20

RESULT 7
 US-09-267-574-21
 ; Sequence 21, Application US/09267574
 ; Patent No. 639571
 ; GENERAL INFORMATION:
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Tjoelker, Larry W.
 ; TITLE OF INVENTION: CHITINASE CHITIN-BINDING FRAGMENTS
 ; FILE REFERENCE: 27866/35407
 ; CURRENT FILING DATE: 1999-03-12
 ; EARLIER APPLICATION NUMBER: 09/039,198
 ; EARLIER FILING DATE: 1998-03-12
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: Patent Ver. 2.0
 ; SEQ ID NO 21
 ; LENGTH: 35
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: primer
 US-09-267-574-21

Query Match 65.0%; Score 13; DB 4; Length 35;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 13: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TTCCGAGAGCTTG 14
 |||||
 Db 8 TTCCGAGAGCTTG 20

RESULT 8
 US-09-023-082A-40/c
 ; Sequence 40, Application US/09023082A
 ; Patent No. 6077692
 ; GENERAL INFORMATION:
 ; APPLICANT: RUBEN, STEVEN M.
 ; APPLICANT: JIMENEZ, PABLO
 ; APPLICANT: DUAN, D. ROXANNE
 ; APPLICANT: RAMPY, MARK A.
 ; APPLICANT: MENDRICK, DONNA
 ; APPLICANT: ZHANG, JUN
 ; APPLICANT: NI, JIAN
 ; APPLICANT: MOORE, PAUL A.
 ; APPLICANT: COLEMAN, TIMOTHY A.
 ; APPLICANT: GRUBER, JOACHIM R.
 ; APPLICANT: DILLON, PATRICK J.
 ; APPLICANT: GENTZ, REINER L.
 ; TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
 ; NUMBER OF SEQUENCES: 148
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
 ; STREET: 1100 NEW YORK AVE, NW, SUITE 600
 ; CITY: WASHINGTON
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/023,082A
 ; FILING DATE: 13-FEB-1998

CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/01790
 ; FILING DATE: 14-FEB-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/461,195
 ; FILING DATE: 05-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/023,852
 ; FILING DATE: 13-AUG-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/039,045
 ; FILING DATE: 28-FEB-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/862,432
 ; FILING DATE: 23-MAY-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/910,875
 ; FILING DATE: 13-AUG-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/055,561
 ; FILING DATE: 13-AUG-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: STEFFE, ERIC K.
 ; REGISTRATION NUMBER: 36,688
 ; REFERENCE/DOCKET NUMBER: 1488.0360008/EKS
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 40:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 38 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: CDNA
 US-09-023-082A-40

Query Match 62.0%; Score 12.4; DB 3; Length 38;
 Best Local Similarity 92.9%; Pred. No. 1.3e+03;
 Matches 13: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 CCCAGAGCTTGCA 17
 |||||
 Db 24 CCCAGAGCTTGCA 11

RESULT 9
 US-09-344-579-22
 ; Sequence 22, Application US/09344579
 ; Patent No. 6054316
 ; GENERAL INFORMATION:
 ; APPLICANT: Brenda F. Baker
 ; APPLICANT: Lex M. Cowsett
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF ETS-2 EXPRESSION
 ; FILE REFERENCE: RTS-0063
 ; CURRENT APPLICATION NUMBER: US/09/344,579
 ; CURRENT FILING DATE: 1999-06-25
 ; NUMBER OF SEQ ID NOS: 47
 ; SEQ ID NO 22
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-09-344-579-22

Query Match 61.0%; Score 12.2; DB 3; Length 18;
 Best Local Similarity 82.4%; Pred. No. 1.5e+03;
 Matches 14: Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GTTCCGAGAGCTTGCA 17
 |||||

DB 2 GTCCGACAGATCTCA 18

RESULT 10
US-08-358-782D-5
Sequence 5, Application US/08358782D
Patent No. 5674682
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Gonnella, Leonard
APPLICANT: Mulholland, S. Grant
APPLICANT: Moreno, Jose
APPLICANT: Fischer, Rainer
TITLE OF INVENTION: Methods of Detecting Micrometastasis of Prostate
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
STREET: One Liberty Place 46th. Floor
CITY: Philadelphia
STATE: PA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,782D
FILING DATE: 15-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: TJU-1327
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-358-782D-5

Query Match 61.0%; Score 12.2; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 CCCAGAGCTTGCACCT 20
DB 3 CCCAGAGCTTGCACCT 19

RESULT 11
US-08-764-527A-5
Sequence 5, Application US/08764527A
Patent No. 5939258
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Gonnella, Leonard
APPLICANT: Mulholland, S. Grant
APPLICANT: Moreno, Jose
APPLICANT: Fischer, Rainer
TITLE OF INVENTION: Methods of Detecting Micrometastasis of
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
STREET: One Liberty Place 46th. Floor

CITY: Philadelphia
STATE: PA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,527A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/358,782
FILING DATE: 15-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: TJU-1327
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-764-527A-5

Query Match 61.0%; Score 12.2; DB 2; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 CCCAGAGCTTGCACCT 20
DB 3 CCCAGAGCTTGCACCT 19

RESULT 12
US-08-066-325-5
Sequence 5, Application US/08066325
Patent No. 5667967
GENERAL INFORMATION:
APPLICANT: Steinman, Lawrence
APPLICANT: Oksenberg, Jorge
APPLICANT: Bernard, Claude
TITLE OF INVENTION: T-CELL RECEPTOR VARIABLE TRANSCRIPTS AS DISEASE RELATED MAR
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fitch Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/066,325
FILING DATE: 21-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5667967tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 690068,408C1
TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-066-325-5

Query Match 61.0%; Score 12.2; DB 1; Length 24;
Best Local Similarity 82.4%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GTTCCAGAGCTTGCCT 17
Db 3 GTTCCAGAGAGGAGCA 19

RESULT 13
US-08-483-316-5
Sequence 5, Application US/08483316
Patent No. 6045802
GENERAL INFORMATION:
APPLICANT: SCHLOW, JEFFREY
APPLICANT: KANTOR, JUDITH
TITLE OF INVENTION: ENHANCED IMMUNE RESPONSE
TITLE OF INVENTION: TO AN ANTIGEN BY A COMPOSITION OF A
TITLE OF INVENTION: RECOMBINANT VIRUS EXPRESSING THE ANTIGEN WITH
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,316
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/317,268
FILING DATE: 03-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWN, KATHRYN M.
REGISTRATION NUMBER: 34,556
REFERENCE/DOCKET NUMBER: 2026-4176051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: yes
AMT1-SENSE: NO
US-08-483-316-5

Query Match 61.0%; Score 12.2; DB 3; Length 28;
Best Local Similarity 82.4%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 CCCAGAGCTTGCACCT 20
Db 9 CCCAGAGCTTACACCT 25

RESULT 14
US-08-500-306-1
Sequence 1, Application US/08500306
Patent No. 615460
GENERAL INFORMATION:
APPLICANT: SCHLOW, JEFFREY
APPLICANT: PANICALLI, DENNIS
TITLE OF INVENTION: GENERATION OF IMMUNE RESPONSES TO
TITLE OF INVENTION: PROSTATE-SPECIFIC ANTIGEN (PSA)
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEWALL, P. BRONSTEIN, DIKE, BRONSTEIN,
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: US
ZIP: 02129
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500,306
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
US-08-500-306-1

Query Match 61.0%; Score 12.2; DB 4; Length 28;
Best Local Similarity 82.4%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 CCCAGAGCTTGCACCT 20
Db 9 CCCAGAGCTTACACCT 25

RESULT 15
US-09-521-668B-7
Sequence 7, Application US/09521668B
Patent No. 6303383
GENERAL INFORMATION:
APPLICANT: NAKAMURA, JUN
APPLICANT: KANNO, SOHEI
APPLICANT: KIMURA, EITICHIRO
APPLICANT: MATSUI, KAOHIKO
APPLICANT: NAKAMATSU, TSUYOSHI
TITLE OF INVENTION: TEMPERATURE SENSITIVE PLASMID FOR CORYNEFORM BACTERIA
FILE REFERENCE: 0010-1093-0
CURRENT APPLICATION NUMBER: US/09/521,668B
CURRENT FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: JP 11-69896
PRIOR FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 20

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OM nucleic - nucleic search, using sw model

Run on: November 28, 2002, 15:32:44 : Search time 185.517 Seconds
(without alignments)
242.780 Million cell updates/sec

Title: US-09-719-737-2

Perfect score: 20

Sequence: 1 gttccagagctgccacct 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
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15: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
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21: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	100.0	20	21	AA256186		Antisense oligonucleotide
2	13.8	69.0	17	AA256186		Reverse primer #12
3	13.6	68.0	25	AA167449		Probe sequence use
4	13.6	68.0	25	AAH22292		Tissue factor path
5	13.4	67.0	17	AAV95349		Human c-fos target
6	13.4	67.0	20	AA256186		Human c-fos oligo
7	13.4	67.0	20	AA256186		Human c-fos oligo
8	13.2	66.0	20	AA195431		Capture oligonucleotide
9	13.2	66.0	24	AA187432		Capture oligonucleotide

C	10	13.2	66.0	24	24	AB187433	Capture oligonucleotide
C	11	13.2	66.0	24	24	AB188068	Capture oligonucleotide
C	12	13.2	66.0	24	24	AB188069	Capture oligonucleotide
C	13	13.2	66.0	28	10	AA91567	Neisseria gonorrhoea
C	14	13.2	66.0	28	10	AA91568	Neisseria gonorrhoea
C	15	13.2	66.0	28	10	AA91569	Neisseria gonorrhoea
C	16	13.2	66.0	28	10	AA91570	Neisseria gonorrhoea
C	17	13.2	66.0	15	22	AA69385	Human ILKAP gene
C	18	13.2	66.0	35	20	AA20957	Mouse adipose prot
C	19	12.8	64.0	24	24	AB16791	Antisense oligonucleotide
C	20	12.8	64.0	25	21	AA57806	Oligonucleotide for
C	21	12.8	64.0	26	24	AB075836	Human NPAT protein
C	22	12.8	64.0	41	24	AB075836	PCR primer used to
C	23	12.8	64.0	44	20	AA26321	Human DSS2169 locu
C	24	12.8	64.0	50	22	AA177541	Human DSS2169 locu
C	25	12.6	63.0	20	24	AA36387	Human gene single
C	26	12.6	63.0	21	22	AA97155	Human gene single
C	27	12.6	63.0	25	22	AA97155	BAP28 gene fragmen
C	28	12.6	63.0	25	22	AA97155	Spinach chloroplast
C	29	12.6	63.0	28	21	AA08335	Soluble sc-TFR fus
C	30	12.6	63.0	39	20	AA55433	T. gondii MGIS4-4
C	31	12.4	62.0	19	20	AA91414	Sequencing primer
C	32	12.4	62.0	19	22	AA542737	Human gene single
C	33	12.4	62.0	21	22	AA96776	Polymorphic fragme
C	34	12.4	62.0	29	21	AA04539	P. patens cell cyc
C	35	12.4	62.0	32	24	AA167524	Cell cycle (CC-2)
C	36	12.4	62.0	32	24	AA167524	PCR primer for mut
C	37	12.4	62.0	38	19	AA167532	PCR primer for E.C
C	38	12.4	62.0	38	20	AA167532	Human KGF-2 E. col
C	39	12.4	62.0	38	21	AA11115	PCR primer #1 for
C	40	12.4	62.0	48	24	AA31922	Streptococcus agal
C	41	12.4	62.0	48	24	AA31922	Human Ets-2 phosph
C	42	12.2	61.0	18	21	AA38363	Prostate specific
C	43	12.2	61.0	19	18	AA91048	PCR primer for pro
C	44	12.2	61.0	19	20	AA91048	Prostate specific
C	45	12.2	61.0	20	20	AA87283	Prostate specific

ALIGNMENTS

RESULT 1
AA256186 standard; DNA: 20 BP.
XX AC AA256186;
XX DT 28-MAR-2000 (first entry)
XX DE Antisense oligonucleotide OD2 for inhibiting IL-4 receptor expression.
XX KW Interleukin-4; IL-4; antisense oligonucleotide; asthma; allergy; cancer;
XX KM receptor expression inhibitor; Immunoglobulin E; IGE; inflammation;
XX KW hyperosteorhiza; ss.
XX OS Homo sapiens.
XX XX MO9966037-A2.
XX PD 23-DEC-1999.
XX PF 17-JUN-1999; 99MO-CA00572.
XX PR 17-JUN-1998; 98CA-2235420.
XX PA (REEX-) RECH EXPERTISES & DEV MEDICAUX PARENZ IN.
XX PI Renzi P;
XX DR WPI: 2000-097743/08.
XX PT Antisense oligonucleotides directed to CCR3, interleukin or granulocyte
PT macrophage colony stimulating factor receptors, used for treating or

PT preventing asthma, allergies, hypercosinophilia, inflammation or cancer
 PS Clalm 5; Page 17; 72pp; English.
 XX
 CC This is an antisense oligonucleotide directed against the interleukin-4
 CC (IL-4) receptor, for inhibiting receptor expression. IL-4 is involved in
 CC immunoglobulin E (IgE) production, the development and persistence of
 CC asthma and atopy. The invention relates to antisense oligonucleotides
 CC directed against a nucleic acid sequence encoding either a chemokine
 CC receptor (CCR3), a common subunit of interleukin-4 (IL-4) and
 CC interleukin-13 (IL-13) receptors, or a common subunit of interleukin-3
 CC (IL-3), interleukin-5 (IL-5) and granulocyte macrophage colony
 CC stimulating factor (GM-CSF) receptors. The antisense oligonucleotides can
 CC be used in the treatment or prevention of asthma, allergy,
 CC hypercosinophilia, general inflammation or cancer.
 XX
 SO Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 other;
 Query Match 100.0%; Score 20; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 CTGCCAGACCTTGCCACCT 20
 DB 1 CTGCCAGACCTTGCCACCT 20
 RESULT 2
 AACT3582/c
 ID AACT3582 standard; DNA; 17 BP.
 AC AACT3582;
 XX
 DT 02-FEB-2001 (first entry)
 XX
 DE Reverse primer #128 used in multiplexing PCR/SBE assay.
 XX
 KW Oligonucleotide array; genotyping; single base extension reaction; SBE;
 KW PCR primer; polymorphic locus; single nucleotide polymorphism; ss.
 XX
 OS unidentified.
 XX
 PA WO200058516-A2.
 PN
 XX
 PD 05-OCT-2000.
 XX
 PF 27-MAR-2000; 2000MO-US08069.
 XX
 PR 26-MAR-1999; 99US-0126473.
 PR 23-JUN-1999; 99US-0140359.
 XX
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA (AFRY-) AFFYMETRIX INC.
 XX
 PI Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;
 PI Ryder T, Sklar P;
 XX
 DR WPI: 2000-656171/63.
 XX
 PT Universal array of oligonucleotides tags attached to a solid substrate
 PT along with locus-specific tagged oligonucleotides useful in genotyping
 PT using single base extension reactions
 XX
 PS Example 7; Page 62; 83pp; English.
 CC The present invention relates to an oligonucleotide array comprising
 CC oligonucleotide tags fixed to a solid substrate. The oligonucleotide
 CC array is useful for genotyping a nucleic acid sample at one or more loci
 CC via single base extension (SBE) reactions. A pair of primers is used to
 CC amplify a polymorphic locus in a sample e.g. a single nucleotide
 CC polymorphism (SNP). The present sequence is one of the primers used in
 CC the method of the present invention to amplify a polymorphic sample. The

CC amplified nucleic acid product is then used as a template in a SBE
 CC reaction with an extension primer. The SBE reaction products are used to
 CC form the oligonucleotide array.
 XX
 SO Sequence 17 BP; 4 A; 3 C; 7 G; 3 T; 0 other;
 Query Match 69.0%; Score 13.8; DB 21; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.7e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 4 CCCGACCTTGCCACCT 20
 DB 17 CCCGACCTTGCCACCT 1
 RESULT 3
 AA167449
 ID AA167449 standard; DNA; 25 BP.
 AC AA167449;
 XX
 DT 11-FEB-2002 (first entry)
 XX
 DE Probe sequence used for real-time RT-PCR analysis.
 XX
 KW ARP; angiogenesis; vascular endothelial growth factor; VEGF; cytoskeletal;
 KW arginine-rich protein; cardanol; antiatherosclerotic; antiatheritic; human;
 KW antiatherosclerotic; vasotrophic; gynecological; antidiabetic; vulvular;
 KW anticancer; dermatological; ophthalmological; antipsoriatic; apoptosis;
 KW gene therapy; RT-PCR; primer; ss.
 XX
 OS Synthetic.
 XX
 PA WO200170174-A2.
 PN
 XX
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001MO-US09043.
 XX
 PR 21-MAR-2000; 2000US-191201P.
 XX
 PA (CURA-) CURAGEN CORP.
 PA (GETH) GENENTECH INC.
 XX
 PI Rastelli LK, Gerber H;
 XX
 DR WPI: 2001-639087/73.
 XX
 PT Modulating angiogenesis and/or apoptosis for preventing or treating
 PT cancer, myocardial infarction and promoting healing, by modulating the
 PT activity of vascular endothelial growth factor-modulated gene
 PT polypeptide -
 XX
 PS Example 2; Page 103; 155pp; English.
 XX
 CC The invention relates to modulating angiogenesis and cell survival that
 CC involves modulating the activity of at least one vascular endothelial
 CC growth factor (VEGF)-modulated gene polypeptide. The method is useful for
 CC modulating angiogenesis and cell survival, for treating tumour and cancer
 CC by decreasing angiogenesis in cancerous tumours and treating myocardial
 CC infarction and promoting healing, by increasing angiogenesis. Transgenic
 CC non-human animals, having disrupted arginine-rich protein (ARP), are
 CC useful for determining the clinical stage of ovarian tumours, which is
 CC useful for determining if the tumour has potential for metastasis. ARP is
 CC useful in gene therapy and in diagnostic applications. VEGFm proteins
 CC are useful in the treatment of tumours, neoplasias, hemangiomas,
 CC rheumatoid arthritis, atherosclerosis, idiopathic pulmonary fibrosis,
 CC vascular restenosis, arteriovenous malformations, meningioma, neovascular
 CC glaucoma, psoriasis, hemophilic joints, hypertrophic scars, Geller-Weber
 CC syndrome, scleroderma, vascular adhesion pathology, synovitis,
 CC dermatitis, endometriosis, diabetic retinopathy, neovascularization
 CC associated with corneal injury or grafts, wound, sore, and ulcer healing.
 CC Sequences AA167449-487 represent probe primer sets used for real-time

CC RT-PCR analysis of differential gene expression.
XX Sequence 25 BP; 6 A; 7 C; 6 G; 6 T; 0 other;
SQ

Query Match 68.0%; Score 13.6; DB 22; Length 25;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTTCCGACGCTTGCACCT 20
||||||| 11 1111 11
Db 4 GTTCCCAAGTTGCCGCGCT 23

RESULT 4
AAH22292
ID AAH22292 standard; DNA; 25 BP.
XX
XX AAH22292;
XX
XX 21-AUG-2001 (first entry)
XX
XX Tissue factor pathway inhibitor-2 hybridisation probe SEQ ID NO:38.
DE
XX Human; differentially expressed gene; angiogenesis; diagnosis;
XX angiogenic disorder; wound healing; cancer; cardiovascular; psoriasis;
XX vascular tumour; proliferative tumour; proliferative vitreoretinopathy;
XX rheumatoid arthritis; Crohn's disease; atherosclerosis; endometriosis;
XX neovascularisation; restenosis; hypertension; aneurysm; angina;
XX myocardial infarction; chronic heart condition; osteoporosis;
XX PCR primer; hybridisation; probe; ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
XX WO200132926-A2.
XX
XX 10-MAY-2001.
XX
XX 01-NOV-2000; 2000WO-US0051.
XX
XX 01-NOV-1999; 99US-016269.
PR 13-APR-2000; 2000US-0196802.
PR 31-OCT-2000; 2000US-0703350.
XX
XX (CURA-) CURAGEN CORP.
PA (GETH) GEMENTECH INC.
XX
XX Mehrahan F, Gerritsen M, Rastelli L;
PI
XX WPI: 2001-291056/30.
DR
XX
XX Differentially expressed genes involved in angiogenesis, useful for
PT treating e.g. vascular tumours, atherosclerosis and/or restenosis
PT subsequent to balloon angioplasty -
XX
XX Example 19; Page 148; 182pp; English.
XX
XX The present invention describes differentially expressed genes involved
CC in angiogenesis (1), and the polypeptides that encode them. (1) have
CC cardiovascular activity, and can be used in the modulation of
CC angiogenesis. The nucleic acids and polypeptides may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate angiogenesis. The polypeptides may also be used as antigens
CC in the production of antibodies against them and in assays to identify
CC modulators of their expression and activity. The antibodies and
CC antagonists may also be used to down regulate expression and activity
CC and modulate angiogenesis. The antibodies may also be used as diagnostic
CC agents for detecting the presence of the polypeptides in samples.
CC Disorders that may be prevented, diagnosed and/or treated by the above
CC methods include, for example vascular tumours, proliferative tumours,
CC proliferative vitreoretinopathy, rheumatoid arthritis, Crohn's disease,
CC atherosclerosis, ovarian hyperstimulation, psoriasis, endometriosis
CC associated with neovascularisation, restenosis subsequent to balloon

CC angioplasty, scar tissue over production, peripheral vascular disease,
CC hypertension, inflammatory vasculitis, Reynaud's disease and
CC Reynaud's phenomenon, aneurysms, arterial restenosis, thrombophlebitis,
CC lymphangitis, lymphedema, wound healing and tissue repair, ischemia
CC reperfusion injury, angina, myocardial infarctions, chronic heart
CC conditions, heart failure such as congestive heart failure, age-related
CC macular degeneration and osteoporosis. AAH22255 to AAH22325 and AAB98322
CC to AAB98325 represent sequence used in the exemplification of the
CC present invention.
XX
XX Sequence 25 BP; 6 A; 7 C; 6 G; 6 T; 0 other;
SQ

Query Match 68.0%; Score 13.6; DB 22; Length 25;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTTCCGACGCTTGCACCT 20
||||||| 11 1111 11
Db 4 GTTCCCAAGTTGCCGCGCT 23

RESULT 5
AAV95349
ID AAV95349 standard; RNA; 17 BP.
XX
XX AAV95349;
XX
XX 24-FEB-1999 (first entry)
XX
XX Human c-fos target sequence nucleotide position 845.
DE
XX
XX Human; c-fos; hammerhead ribozyme; hairpin ribozyme; target site;
XX cancer; oncogene; leukaemia; neuroblastoma; diagnosis; genetic drift;
XX mutation; diseased cell; ss.
XX
XX Homo sapiens.
OS
XX WO9832846-A2.
XX
XX 30-JUL-1998.
XX
XX 20-JAN-1998; 98WO-US01017.
XX
XX 23-JAN-1997; 97US-0037658.
PR
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX
XX Jarvis T, McSwiggen JA, Stinchcomb DF;
PI
XX WPI: 1998-427942/36.
DR
XX
XX Enzymatic nucleic acid molecules which specifically cleave RNA
PT derived from a c-fos gene - useful for treating conditions related
PT to levels of c-fos, especially cancer
XX
XX Claim 2; Page 51; 72pp; English.
XX
XX The present invention describes an enzymatic nucleic acid molecule which
CC specifically cleaves RNA derived from a c-fos gene. AAV95401 to AAV95340
CC and AAV95541 to AAV95584 represent hammerhead ribozymes and hairpin
CC ribozymes, respectively, which specifically cleave human c-fos target
CC to AAV95400 and AAV95585 to AAV95628 represent human c-fos target
CC sequences. The enzymatic nucleic acid molecules can be used for treating
CC cancer associated with elevated levels of c-fos oncogene, especially
CC leukaemias, neuroblastomas and lung, breast and colon cancers. The
CC ribozymes may also be used as diagnostic tools to examine genetic drift
CC and mutations within diseased cells, or to detect the presence of c-fos
CC RNA in a cell.
XX
XX Sequence 17 BP; 3 A; 8 C; 4 G; 2 U; 0 other;
SQ

Query Match 67.0%; Score 13.4; DB 19; Length 17;
Best Local Similarity 80.0%; Pred. No. 2.7e+03;

Matches 12: Conservative 2: Mismatches 1: Indels 0: Gaps 0:
QY 5 CCAGAGCTTGGCACC 19
|||||:|||||
DB 1 CCAGAGCTTGGCACC 15

RESULT 6
AAC83618/c
ID AAC83618 standard; DNA: 20 BP.

XX AAC83618;

XX 27-FEB-2001 (first entry)

XX Human c-fos oligo DNA D3.

XX Human; c-fos; fluorescent probe; cytoplasmic nucleic acid detection; ss.

XX Homo sapiens.

XX EPI052293-A1.

XX 15-NOV-2000.

XX 27-DEC-1999; 99EP-0126030.

XX 12-MAY-1999; 99JP-0131838.

XX (MOLE-) LAB MOLECULAR BIOPHOTONICS.

XX Tsuji A, Hirano M, Koshimoto H, Ishibashi K;

XX WPI; 2001-018062/03.

PT Detection of a target nucleic acid in the cytoplasm of a living cell
comprises using a fluorescent probe linked to a component that cannot
permeate through the nuclear membrane -

XX Example 1; Page 11; 53pp; English.

CC The present sequence is a probe which was used in a method for nucleic
acid detection in cytoplasm. The method comprises detecting a target
nucleic acid using a fluorescent hybridisation probe linked to a
component that cannot permeate through the nuclear membrane of the
cell. The present sequence was used for detecting cytoplasmic human
c-fos mRNA molecules. The detection probe of this method is not
readily degraded by endogenous cytoplasmic nucleases unlike currently
available detection probes, as it has a specified structure which does
not rapidly move to the nucleus when introduced into the cytoplasm of a
living cell.

XX Sequence 20 BP; 2 A; 6 C; 8 G; 4 T; 0 other;

Query Match 67.0%; Score 13.4; DB 22: Length 20;

Best Local Similarity 93.3%; Pred. No. 2.7e+03;

Matches 14: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCAGAGCTTGGCACC 19
|||||:|||||

DB 20 CCAGAGCTTGGCACC 6

RESULT 7
AAC83624/c

ID AAC83624 standard; DNA: 20 BP.

XX AAC83624;

XX 27-FEB-2001 (first entry)

XX Human c-fos Bodipy493/503-labelled oligo DNA D3F.

KW Human; c-fos; fluorescent probe; cytoplasmic nucleic acid detection; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FH modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note="attached to fluorescent dye Bodipy493/503"

XX EPI052293-A1.

XX 15-NOV-2000.

XX 27-DEC-1999; 99EP-0126030.

XX 12-MAY-1999; 99JP-0131838.

XX (MOLE-) LAB MOLECULAR BIOPHOTONICS.

XX Tsuji A, Hirano M, Koshimoto H, Ishibashi K;

XX WPI; 2001-018062/03.

PT Detection of a target nucleic acid in the cytoplasm of a living cell
comprises using a fluorescent probe linked to a component that cannot
permeate through the nuclear membrane -

XX Example 1; Page 13; 53pp; English.

CC The present sequence is a probe which was used in a method for nucleic
acid detection in cytoplasm. The method comprises detecting a target
nucleic acid using a fluorescent hybridisation probe linked to a
component that cannot permeate through the nuclear membrane of the
cell. The present sequence was used for detecting cytoplasmic human
c-fos mRNA molecules. The detection probe of this method is not
readily degraded by endogenous cytoplasmic nucleases unlike currently
available detection probes, as it has a specified structure which does
not rapidly move to the nucleus when introduced into the cytoplasm of a
living cell.

XX Sequence 20 BP; 2 A; 6 C; 8 G; 4 T; 0 other;

Query Match 67.0%; Score 13.4; DB 22: Length 20;

Best Local Similarity 93.3%; Pred. No. 2.7e+03;

Matches 14: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCAGAGCTTGGCACC 19
|||||:|||||

DB 20 CCAGAGCTTGGCACC 6

RESULT 8
AB195431

ID AB195431 standard; DNA: 20 BP.

XX AB195431;

XX 16-FEB-2002 (first entry)

XX Capture oligonucleotide Zhp ID#2518 oligo #9.

XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;

XX lligase detection reaction; LDR; p53; BRCA1; BRCA2; Infectious disease;

XX cancer; oncogene; tumour suppressor; human papillomavirus; forensic;

XX environmental monitoring; food industry; feed industry; ss.

XX Synthetic.

XX WO200179548-A2.

XX 25-OCT-2001.

```
XX 04-APR-2001: 2001WO-US10958.
XX 14-APR-2000: 2000US-197271P.
XX (CORR ) CORNELL RES FOUND INC.
XX PI Barany F, Zilvi M, Gerry NP, Favis R, Kliman R;
XX WPI: 2002-034366/04.
XX
XX Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch -
XX
XX Example 5: Fig 29: 300pp; English.
XX
XX The present invention describes a method (M1) for designing capture
XX oligonucleotide probes (I) for use on a support to which complementary
XX oligonucleotide probes (II) will hybridise with little mismatch, where
XX (I) have melting temperatures within a narrow range. The method is useful
XX for detecting infectious diseases caused by bacterial infectious agents
XX e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
XX infectious agents e.g. Cryptococcus neoformans, Candida albicans and
XX Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
XX Epstein-Barr virus and polio virus, and parasitic infectious agents
XX selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
XX medinensis. The method is also useful for detecting genetic diseases such
XX as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
XX Detecting cancer involving oncogenes, tumour suppressor genes, or genes
XX involved in DNA amplification, replication, recombination or repair, the
XX cancer is specifically associated with a gene selected from BRCA1 gene,
XX p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
XX method is also used for environmental monitoring, forensics and the food
XX and feed industry, detecting comprises scanning (using e.g. a scanning
XX electron microscope and infrared microscope) the support at the
XX particular sites and identifying if ligation of the oligonucleotide probe
XX sets occurred and correlating (using a computer) identified ligation to a
XX presence or absence of the target nucleotide sequences. AB182074 to
XX CC AB197546 represent oligonucleotide sequences used in the exemplification
XX of the present invention.
XX
XX Sequence 20 BP: 3 A: 9 C: 3 G: 5 T: 0 other:
XX
XX Query Match 66.0% Score 13.2: DB 24: Length 20:
XX Best Local Similarity 83.3%: Pred. No. 3.4e+03:
XX Matches 15: Conservative 0: Mismatches 3: Indels 0: Gaps 0:
XX
XX QY 3 TCCGAGACCTTGCCACCT 20
XX ||||| || ||||| ||
XX Db 1 TCCGAGACCTTGCCATCT 18
XX
XX RESULT 9
XX AB187432
XX ID AB187432 standard; DNA: 24 BP.
XX
XX AC AB187432:
XX
XX DT 15-FEB-2002 (first entry)
XX
XX DE Capture oligonucleotide zlp ID#2518 oligo #1.
XX
XX KM Human: K-ras; PCR primer; probe; capture probe; mutation detection;
XX KM ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
XX KM infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
XX KM cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
XX KM environmental monitoring; food industry; feed industry; ss.
XX
XX OS Synthetic.
XX
XX PN WO200179548-A2.
XX
XX XX 25-OCT-2001.
```

```
XX 04-APR-2001: 2001WO-US10958.
XX 14-APR-2000: 2000US-197271P.
XX (CORR ) CORNELL RES FOUND INC.
XX PI Barany F, Zilvi M, Gerry NP, Favis R, Kliman R;
XX WPI: 2002-034366/04.
XX
XX Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch -
XX
XX Example 5: Fig 25: 300pp; English.
XX
XX The present invention describes a method (M1) for designing capture
XX oligonucleotide probes (I) for use on a support to which complementary
XX oligonucleotide probes (II) will hybridise with little mismatch, where
XX (I) have melting temperatures within a narrow range. The method is useful
XX for detecting infectious diseases caused by bacterial infectious agents
XX e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
XX infectious agents e.g. Cryptococcus neoformans, Candida albicans and
XX Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
XX Epstein-Barr virus and polio virus, and parasitic infectious agents
XX selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
XX medinensis. The method is also useful for detecting genetic diseases such
XX as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
XX Detecting cancer involving oncogenes, tumour suppressor genes, or genes
XX involved in DNA amplification, replication, recombination or repair, the
XX cancer is specifically associated with a gene selected from BRCA1 gene,
XX p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
XX method is also used for environmental monitoring, forensics and the food
XX and feed industry, detecting comprises scanning (using e.g. a scanning
XX electron microscope and infrared microscope) the support at the
XX particular sites and identifying if ligation of the oligonucleotide probe
XX sets occurred and correlating (using a computer) identified ligation to a
XX presence or absence of the target nucleotide sequences. AB182074 to
XX CC AB197546 represent oligonucleotide sequences used in the exemplification
XX of the present invention.
XX
XX Sequence 24 BP: 4 A: 10 C: 4 G: 6 T: 0 other:
XX
XX Query Match 66.0% Score 13.2: DB 24: Length 24:
XX Best Local Similarity 83.3%: Pred. No. 3.5e+03:
XX Matches 15: Conservative 0: Mismatches 3: Indels 0: Gaps 0:
XX
XX QY 3 TCCGAGACCTTGCCACCT 20
XX ||||| || ||||| ||
XX Db 1 TCCGAGACCTTGCCATCT 18
XX
XX RESULT 10
XX AB187433/C
XX ID AB187433 standard; DNA: 24 BP.
XX
XX AC AB187433:
XX
XX DT 15-FEB-2002 (first entry)
XX
XX DE Capture oligonucleotide zlp ID#2518 oligo #2.
XX
XX KM Human: K-ras; PCR primer; probe; capture probe; mutation detection;
XX KM ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
XX KM infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
XX KM cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
XX KM environmental monitoring; food industry; feed industry; ss.
XX
XX OS Synthetic.
XX
XX PN WO200179548-A2.
XX
XX XX 25-OCT-2001.
```

XX	PF	04-APR-2001:	2001WO-US10958.
XX	PR	14-APR-2000:	2000US-197271P.
XX	PA	(CORR)	CORNELL RES FOUND INC.
XX	PI	Barany F, Zifra M, Gerry NP, Favis R, Kilman R:	
XX	DR	WPI: 2002-034366/04.	
XX	PT	Designing capture oligonucleotide probes for use on a support to which	
XX	PT	complementary oligonucleotides hybridize with little mismatch -	
XX	PS	Example 5; Fig 25: 300bp: English.	
CC	CC	The present invention describes a method (M1) for designing capture	
CC	CC	oligonucleotide probes (I) for use on a support to which complementary	
CC	CC	oligonucleotide probes (II) will hybridize with little mismatch, where	
CC	CC	(I) have melting temperatures within a narrow range. The method is useful	
CC	CC	for detecting infectious diseases caused by bacterial infectious agents	
CC	CC	e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal	
CC	CC	infectious agents e.g. Cryptococcus neoformans, Candida albicans and	
CC	CC	Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,	
CC	CC	Estein-Barr virus and polio virus, and parasitic infectious agents	
CC	CC	selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus	
CC	CC	medicinis. The method is also useful for detecting genetic diseases such	
CC	CC	as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.	
CC	CC	Detecting cancer involving oncogenes, tumour suppressor genes, or genes	
CC	CC	involved in DNA amplification, replication, recombination or repair, the	
CC	CC	cancer is specifically associated with a gene selected from BRCA1 gene,	
CC	CC	p53 gene, human papillomavirus types 16 and 18 and liver cancers. The	
CC	CC	method is also used for environmental monitoring, forensics and the food	
CC	CC	and feed industry, detecting comprises scanning (using e.g. a scanning	
CC	CC	electron microscope and infrared microscope) the support at the	
CC	CC	particular sites and identifying if ligation of the oligonucleotide probe	
CC	CC	occurred and correlating (using a computer) identified ligation to a	
CC	CC	presence or absence of the target nucleotide sequences. AB182074 to	
CC	CC	AB197546 represent oligonucleotide sequences used in the exemplification	
CC	CC	of the present invention.	
XX	XX	Sequence 24 BP: 6 A; 4 C; 10 G; 4 T; 0 other:	
QY	QY	Query Match	66.0%; Score 13.2; DB 24; Length 24;
DB	DB	Best Local Similarity	83.3%; Pred. No. 3.5e+03;
Matches	Matches	15; Conservative	0; Mismatches 3; Indels 0; Gaps 0.
3	3	TCCGACGCTTGCCACT 20	
24	24	TCCGACGCTTGCCACT 7	
RESULT 11			
AB188068			
AB188068			standard: DNA: 24 BP.
15-FEB-2002			(first entry)
Capture oligonucleotide			21P ID#2836 oligo #1.
Human: K-ras: PCR primer: probe; capture probe; mutation detection;			
Ligase detection reaction: LDR: p33: BRCA1: BRCA2: infectious disease;			
Infection: 21 hydroxylase deficiency; Turner Syndrome; obesity;			
cancer; oncogene; tumour suppressor; human papillomavirus; forensic;			
environmental monitoring; food industry; feed industry; ss.			
Synthetic.			
WO200179548-A2.			
25-OCT-2001			

PF	04-APR-2001:	2001WO-US10958.
XX		
XX	14-APR-2000:	2000US-197271P.
XX		
PA	(CORR)	CORNELL RES FOUND INC.
PA		
PI	Barany F, Zilvi M, Gerry NP, Favis R, Kliman R;	
XX	WPI: 2002-034366/04.	
XX		
DR		
PT	Designing capture oligonucleotide probes for use on a support to which	
PT	complementary oligonucleotides hybridize with little mismatch -	
PS		
XX	Example 5: Fig 25: 300pp: English.	
XX		
CC	The present invention describes a method (M1) for designing capture	
CC	oligonucleotide probes (I) for use on a support to which complementary	
CC	oligonucleotide probes (II) will hybridize with little mismatch, where	
CC	(I) have melting temperatures within a narrow range. The method is useful	
CC	for detecting infectious diseases caused by bacterial infectious agents	
CC	e.g. Salmonella, Listeria monocytogenes and Haemophilus influenzae fungal	
CC	infectious agents e.g. Cryptococcus neoformans, Candida albicans and	
CC	Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,	
CC	Epstein-Barr virus and polio virus, and parasitic infectious agents	
CC	selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus	
CC	melinensis. The method is also useful for detecting genetic diseases such	
CC	as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.	
CC	Detecting cancer involving oncogenes, tumour suppressor genes, or genes	
CC	involved in DNA amplification, replication, recombination or repair, the	
CC	cancer is specifically associated with a gene selected from BRCA1 gene,	
CC	p53 gene, human papillomavirus types 16 and 18 and liver cancers. The	
CC	method is also used for environmental monitoring, forensics and the food	
CC	and feed industry, detecting complises scanning (using e.g. a scanning	
CC	electron microscope and infrared microscope) the support at the	
CC	particular sites and identifying if ligation of the oligonucleotide probe	
CC	sets occurred and correlating (using a computer) identified ligation to a	
CC	presence or absence of the target nucleotide sequences. AD182074 to	
CC	AB197545 represent oligonucleotide sequences used in the exemplification	
CC	of the present invention.	
XX		
SO	Sequence 24 BP: 5 A: 7 C: 6 G: 6 T: 0 other:	
	Query Match	66.0%; Score 13.2; DB 24;
	Best Local Similarity	83.3%; Pred. No. 3.5e+03;
	Matches 15; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
OY	3 TCCGAGACCTTGCACCT 20	
DB	5 TCCCAAGACTTGGCACT 22	
	RESULT 12	
	AB188069/c	
ID	AB188069 standard; DNA: 24 BP.	
AC		
XX	AB188069;	
XX		
DT	15-FEB-2002 (first entry)	
XX		
DE	Capture oligonucleotide zip ID#2836 oligo #2.	
XX		
KW	Human: K-ras: PCR primer; probe: capture probe; mutation detection;	
KW	lyase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;	
KW	Infection; 21 hydroxylase deficiency; Turner Syndrome; Obesity;	
KW	Cancer; oncogene; tumour suppressor; human papillomavirus; forensic;	
XX	environmental monitoring; food industry; feed industry; ss.	
XX		
OS	Synthetic.	
XX		
PN	WO200179548-A2.	
XX		
PD	25-OCT-2001.	

XX 04-APR-2001; 2001WO-US10958.
 PF 14-APR-2000; 2000US-197271P.
 XX
 XX
 PA (CORR) CORNELL RES FOUND INC.
 PI Barany F, Zilvi M, Gerry NP, Favis R, Kilman R;
 XX WPI: 2002-034366/04.
 DR
 XX
 PT Designing capture oligonucleotide probes for use on a support to which
 PT complementary oligonucleotides hybridize with little mismatch -
 XX
 PS Example 5; Fig 25; 300pp; English.
 CC The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridize with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 CC medinensis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. ABR2074 to
 CC ABR17546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention.
 CC
 XX
 SO Sequence 24 BP; 6 A; 6 C; 7 G; 5 T; 0 other;
 Query Match 66.0%; Score 13.2; DB 24;
 Best Local Similarity 83.3%; Pred. No. 3.5e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Caps 0;
 OY 3 TTCCGAGCTTGGCCACT 20
 DB 20 TTCCGAGCTTGGCACT 3

RESULT 13
 AAN91567
 ID AAN91567 standard; DNA; 28 BP.
 XX
 AC AAN91567;
 XX
 DT 02-MAR-1990 (first entry)
 XX
 DE Neisseria gonorrhoea group 17 probe DNA.
 XX
 KW Escherichia coli; probe.
 XX
 OS Neisseria gonorrhoea.
 XX
 PN EP337896-A.
 XX
 PD 18-OCT-1989.
 XX
 PF 14-APR-1989; 89EP-0401045.
 XX
 PR 15-APR-1988; 88EP-0400929.

XX
 PA (INNO) INNOGENETICS NV SA.
 XX
 PI Rossau R, Van Heuverswijn;
 XX
 DR WPI: 1989-302611/42.
 XX
 PT Hybridisation probes for detecting Neisseria strains
 PT - some being specific for Neisseria gonorrhoeae
 XX
 PS Claim 1; page 27; 60pp; English.
 CC This probe, its complementary RNA, or its derivs. can be used to
 CC specifically detect N. gonorrhoea, and can differentiate at the
 CC sub-species level (eliminating Southern blotting).
 CC
 XX
 SO Sequence 28 BP; 10 A; 9 C; 3 G; 6 T; 0 other;
 Query Match 66.0%; Score 13.2; DB 10;
 Best Local Similarity 61.1%; Pred. No. 3.5e+03;
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Caps 0;
 OY 2 TTCCGAGCTTGGCCACC 19
 DB 7 TTCCGAGCTTGGCCACC 24

RESULT 14
 AAN91568
 ID AAN91568 standard; RNA; 28 BP.
 XX
 AC AAN91568;
 XX
 DT 02-MAR-1990 (first entry)
 XX
 DE Neisseria gonorrhoea 17bis probe RNA.
 XX
 KW Escherichia coli; probe.
 XX
 OS Neisseria gonorrhoea.
 XX
 PN EP337896-A.
 XX
 PD 18-OCT-1989.
 XX
 PF 14-APR-1989; 89EP-0401045.
 XX
 PR 15-APR-1988; 88EP-0400929.
 XX
 PA (INNO) INNOGENETICS NV SA.
 XX
 PI Rossau R, Van Heuverswijn;
 XX
 DR WPI: 1989-302611/42.
 XX
 PT Hybridisation probes for detecting Neisseria strains
 PT - some being specific for Neisseria gonorrhoeae
 XX
 PS Claim 1; page 28; 60pp; English.
 CC This probe, its complementary DNA, or its derivs. can be used to
 CC specifically detect N. gonorrhoea, and can differentiate at the
 CC sub-species level (eliminating Southern blotting).
 CC
 XX
 SO Sequence 28 BP; 10 A; 9 C; 3 G; 6 T; 0 other;
 Query Match 66.0%; Score 13.2; DB 10;
 Best Local Similarity 61.1%; Pred. No. 3.5e+03;
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Caps 0;
 OY 2 TTCCGAGCTTGGCCACC 19
 DB 7 TTCCGAGCTTGGCCACC 24

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RESULT 15
AAN91569/C
ID AAN91569 standard; DNA; 28 BP.
XX
AC AAN91569;
XX
CT 02-MAR-1990 (first entry)
XX
DE Neisseria gonorrhoea 17ter probe DNA.
XX
KW Escherichia coli; probe.
XX
OS Neisseria gonorrhoea.
XX
PN EP337896-A.
PD 18-OCT-1989.
XX
PF 14-APR-1989; 89EP-0401045.
XX
PR 15-APR-1988; 88EP-0400929.
XX
PA (INNO ) INNOGENETICS NV SA.
XX
PI Rossau R, Van Heuverswijn;
XX
DR WPI: 1989-302611/42.
XX
PT Hybridisation probes for detecting Neisseria strains
PT - some being specific for Neisseria gonorrhoeae
XX
PS Claim 1; page 28; 60pp; English.
XX
CC This probe, its complementary RNA, or its derivs. can be used to
CC specifically detect N. gonorrhoea, and can differentiate at the
CC sub-species level (eliminating Southern blotting).
XX
SQ Sequence 28 BP; 6 A; 3 C; 9 G; 10 T; 0 other;

Query Match 66.0%; Score 13.2; DB 10; Length 28;
Best Local Similarity 83.3%; pred No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTCCGACGCTTGCAC 19
   ||| | ||||| |
DB 22 TTCCACGACGCTTGCAC 5

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Search completed: November 28, 2002, 17:24:11
 Job time : 186.851 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 28, 2002, 16:42:34 ; Search time 1162.07 Seconds

(Without alignments)
500.879 Million cell updates/sec

Title: US-09-719-737-2

Perfect score: 20
Sequence: 1 gtccccagagctgcacact 20

Scoring table: IDENTITY_NOC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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41: em_hlgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	13.4	67.0	20	AR149434	AR149434 Sequence
3	13.4	67.0	20	AR149440	AR149440 Sequence
4	13.4	67.0	20	E49406	E49406 Method for
5	13.2	66.0	20	E49412	E49412 Method for
6	13.2	66.0	24	AX295389	AX295389 Sequence
7	13.2	66.0	24	AX290756	AX290756 Sequence
8	13.2	66.0	24	AX291074	AX291074 Sequence
9	13.2	66.0	28	A14537	A14537 Group 17 by
10	13.2	66.0	28	A14538	A14538 Group 17 te
11	13.2	66.0	28	A14539	A14539 Group 17 te
12	13.2	66.0	28	A14540	A14540 Group 17 qu
13	13.2	66.0	31	AX248913	AX248913 Sequence
14	13	65.0	35	AR212154	AR212154 Sequence
15	12.8	64.0	24	AX370542	AX370542 Sequence
16	12.8	64.0	26	AX453540	AX453540 Sequence
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18	12.6	63.0	20	AX412207	AX412207 Sequence
19	12.6	63.0	25	AX067206	AX067206 Sequence
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23	12.4	62.0	38	AR099158	AR099158 Sequence
24	12.2	61.0	19	I67855	I67855 Sequence 5
25	12.2	61.0	21	AX096742	AX096742 Sequence
26	12.2	61.0	21	E23807	E23807 Method for
27	12.2	61.0	24	I65283	I65283 Sequence 5
28	12.2	61.0	25	E06786	E06786 Primer. 9/1
29	12.2	61.0	27	AX455026	AX455026 Sequence
30	12.2	61.0	28	AR122021	AR122021 Sequence
31	12.2	61.0	28	AR173104	AR173104 Sequence
32	12.2	61.0	28	AX323159	AX323159 Sequence
33	12.2	61.0	31	AX425940	AX425940 Sequence
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35	12.2	61.0	33	AR098502	AR098502 Sequence
36	12.2	61.0	33	AX441428	AX441428 Sequence
37	12.2	61.0	33	AX453924	AX453924 Sequence
38	12.2	61.0	33	I41462	I41462 Sequence 59
39	12	60.0	21	AX096363	AX096363 Sequence
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43	12	60.0	33	AX004493	AX004493 Sequence
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45	12	60.0	40	BD000662	BD000662 Growth ho

ALIGNMENTS

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DEFINITION Sequence 2 from Patent WO9966037.
ACCESSION AX008649
VERSION AX008649.1 GI:9996173
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

synthetic construct.
artificial sequences.
1 (bases 1 to 20)
Renzl, P.
Antisense oligonucleotides for treating or preventing atopic
diseases and neoplastic cell proliferation
Patent: WO 9966037-A 2 23-DEC-1999;

20 bp
DNA
linear
PAT 06-SEP-2000

Prod. No. is the number of results predicted by chance to have a

REMI PAOLO (CA): RECH EXPERTISES ET DEV MEDICAU (CA)
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/db_xref="taxon:32630"
/note="Antisense oligonucleotide inhibiting the common
subunit of IL-4 and IL-13 human receptor."
BASE COUNT 3 a 8 c 4 g 5 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCCACAGCTTGCACCT 20
|||||
DB 1 GTTCCACAGCTTGCACCT 20

RESULT 2
ARI49434/C
LOCUS ARI49434 5 from patent US 6228592.
DEFINITION Sequence 5 from patent US 6228592.
ACCESSION ARI49434
VERSION ARI49434.1 GI:15114025
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tsuji,A., Hirano,M., Koshimoto,H. and Ishibashi,K.
TITLE Nucleic acid detection in cytoplasm
JOURNAL Patent: US 6228592-A 5 08-MAY-2001;
FEATURES
Source 1. .20
/organism="unknown"
BASE COUNT 2 a 6 c 8 g 4 t
ORIGIN

Query Match 67.0%; Score 13.4; DB 6; Length 20;
Best Local Similarity 93.3%; Pred. No. 5e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 CCACAGCTTGCACCC 19
|||||
DB 20 CCACAGCTTGCACCC 6

RESULT 3
ARI49440/C
LOCUS ARI49440 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 11 from patent US 6228592.
ACCESSION ARI49440
VERSION ARI49440.1 GI:15114031
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tsuji,A., Hirano,M., Koshimoto,H. and Ishibashi,K.
TITLE Nucleic acid detection in cytoplasm
JOURNAL Patent: US 6228592-A 11 08-MAY-2001;
FEATURES
Source 1. .20
/organism="unknown"
BASE COUNT 2 a 6 c 8 g 4 t
ORIGIN

Query Match 67.0%; Score 13.4; DB 6; Length 20;
Best Local Similarity 93.3%; Pred. No. 5e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 CCACAGCTTGCACCC 19

|||||
DB 20 CCACAGCTTGCACCC 6

RESULT 4
E49406/C
LOCUS E49406 20 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for detecting cytoplasmic target nucleic acid in living cell.
E49406
ACCESSION E49406.1 GI:18629305
VERSION E49406.1 GI:18629305
KEYWORDS JP 2001025400-A/5.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tsuji,A., Hirano,M., Koshimoto,H. and Ishibashi,K.
TITLE Method for detecting cytoplasmic target nucleic acid in living cell
JOURNAL Patent: JP 2001025400-A 5 30-JAN-2001;
COMMENT BUNSHI BIO HOTONIKUSU KENKYUSHO
OS Artificial Sequence
PN JP 2001025400-A/5
PD 30-JAN-2001
PF 28-DEC-1999 JP 1999373904
PR AKIHiko TSUJi, MASAHiko HIRANO, HIROYUKI KOSHIMOTO, PI KANAME
PI ISHIBASHI
PC C1201/68,C12N15/09//G01N21/78,C12N15/00

FEATURES
Source 1. .20
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 2 a 6 c 8 g 4 t
ORIGIN

Query Match 67.0%; Score 13.4; DB 6; Length 20;
Best Local Similarity 93.3%; Pred. No. 5e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 CCACAGCTTGCACCC 19
|||||
DB 20 CCACAGCTTGCACCC 6

RESULT 5
E49412/C
LOCUS E49412 20 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for detecting cytoplasmic target nucleic acid in living cell.
E49412
ACCESSION E49412.1 GI:18629311
VERSION E49412.1 GI:18629311
KEYWORDS JP 2001025400-A/11.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tsuji,A., Hirano,M., Koshimoto,H. and Ishibashi,K.
TITLE Method for detecting cytoplasmic target nucleic acid in living cell
JOURNAL Patent: JP 2001025400-A 11 30-JAN-2001;
COMMENT BUNSHI BIO HOTONIKUSU KENKYUSHO
OS Artificial Sequence
PN JP 2001025400-A/11
PD 30-JAN-2001
PF 28-DEC-1999 JP 1999373904
PR AKIHiko TSUJi, MASAHiko HIRANO, HIROYUKI KOSHIMOTO, PI KANAME
PI ISHIBASHI
PC C1201/68,C12N15/09//G01N21/78,C12N15/00


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FEATURES             FH      Key      Location/Qualifiers
                    FT      source      1..20
                    FT      /organism="Artificial Sequence"
FEATURES             source
                    1..20
                    /organism="synthetic construct"
                    /db_xref="taxon:32630"
BASE COUNT          2 a      6 c      8 g      4 t
ORIGIN
Query Match          67.0%; Score 13.4; DB 6; Length 20;
Best Local Similarity 93.3%; Pred. No. 5e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      5 CCAGAGCTTGGCACCT 19
Db      20 CCAGAGCTTGGCACCT 6

RESULT 6
AX295389
LOCUS      AX295389      20 bp      DNA      linear      PAT 21-NOV-2001
DEFINITION Sequence 7151 from Patent WO0179548.
ACCESSION AX295389
VERSION    AX295389.1 GI:17057078
KEYWORDS
SOURCE      synthetic construct.
            synthetic construct.
            artificial sequences.
FEATURES
REFERENCE    1
AUTHORS      Barany,F., Zivvi,M., Gerry,N.P., Favis,R. and Kilman,R.
TITLE        Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
            Patent: WO 0179548-A 7151 25-OCT-2001;
JOURNAL      CORNELL RESEARCH FOUNDATION, INC. (US)
            Location/Qualifiers
FEATURES
source      1..20
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            /note="Hypothetical Probe Sequence"
BASE COUNT          3 a      9 c      3 g      5 t
ORIGIN
Query Match          66.0%; Score 13.2; DB 6; Length 20;
Best Local Similarity 83.3%; Pred. No. 6.4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      3 TCCGAGAGCTTGGCACCT 20
Db      1 TCCGAGAGCTTGGCACCT 18

RESULT 7
AX290756
LOCUS      AX290756      24 bp      DNA      linear      PAT 21-NOV-2001
DEFINITION Sequence 2518 from Patent WO0179548.
ACCESSION AX290756
VERSION    AX290756.1 GI:17052439
KEYWORDS
SOURCE      synthetic construct.
            synthetic construct.
            artificial sequences.
FEATURES
REFERENCE    1
AUTHORS      Barany,F., Zivvi,M., Gerry,N.P., Favis,R. and Kilman,R.
TITLE        Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
            Patent: WO 0179548-A 2518 25-OCT-2001;
JOURNAL      CORNELL RESEARCH FOUNDATION, INC. (US)
            Location/Qualifiers
FEATURES
source      1..24
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            /note="Hypothetical Probe Sequence"

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BASE COUNT          4 a      10 c      4 g      6 t
ORIGIN
Query Match          66.0%; Score 13.2; DB 6; Length 24;
Best Local Similarity 83.3%; Pred. No. 6.3e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      3 TCCGAGAGCTTGGCACCT 20
Db      1 TCCGAGAGCTTGGCACCT 18

RESULT 8
AX291074
LOCUS      AX291074      24 bp      DNA      linear      PAT 21-NOV-2001
DEFINITION Sequence 2836 from Patent WO0179548.
ACCESSION AX291074
VERSION    AX291074.1 GI:17052757
KEYWORDS
SOURCE      synthetic construct.
            synthetic construct.
            artificial sequences.
FEATURES
REFERENCE    1
AUTHORS      Barany,F., Zivvi,M., Gerry,N.P., Favis,R. and Kilman,R.
TITLE        Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
            Patent: WO 0179548-A 2836 25-OCT-2001;
JOURNAL      CORNELL RESEARCH FOUNDATION, INC. (US)
            Location/Qualifiers
FEATURES
source      1..24
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            /note="Hypothetical Probe Sequence"
BASE COUNT          5 a      7 c      6 g      6 t
ORIGIN
Query Match          66.0%; Score 13.2; DB 6; Length 24;
Best Local Similarity 83.3%; Pred. No. 6.3e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      3 TCCGAGAGCTTGGCACCT 20
Db      5 TCCGAGAGCTTGGCACCT 22

RESULT 9
A14537
LOCUS      A14537      28 bp      DNA      linear      PAT 29-SEP-1994
DEFINITION Group 17 hybridization probe for detecting Neisseria strains.
ACCESSION A14537
VERSION    A14537.1 GI:640858
KEYWORDS
SOURCE      synthetic construct.
            synthetic construct.
            artificial sequences.
FEATURES
REFERENCE    1 (bases 1 to 28)
AUTHORS      Rossau,R. and Van Heuverswijn,H.
TITLE        Hybridization probes for detecting neisseria strains
            Patent: EP 0337896-A 68 18-OCT-1989;
JOURNAL      N.V. INNOGENETICS S.A
            Location/Qualifiers
FEATURES
source      1..28
            /organism="synthetic construct"
            /db_xref="taxon:32630"
BASE COUNT          10 a      9 c      3 g      6 t
ORIGIN
Query Match          66.0%; Score 13.2; DB 6; Length 28;
Best Local Similarity 83.3%; Pred. No. 6.3e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      2 TTCCAGAGCTTGGCACCT 19
            ||||| 1 |||||||| 1

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Db 7 TTCCACACGCTTCCCAAC 24

RESULT 10

LOCUS A14538 28 bp DNA linear PAT 29-SEP-1994

DEFINITION Group 17 bis hybridization probe for detecting Neisseria strains.

ACCESSION A14538

VERSION A14538.1 GI:640859

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 28)

AUTHORS Rosseau,R. and Van Heuverswijn,H.

TITLE Hybridization probes for detecting neisseria strains

JOURNAL Patent: EP 0337896-A 69 18-OCT-1989;

N.V. INNOGENETICS S.A

FEATURES

source

1..28

Location/Qualifiers

BASE COUNT 10 a 9 c 3 g 6 t

ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 28;

Best Local Similarity 83.3%; Pred. No. 6.3e+04;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 TTCCACACGCTTCCCAAC 19

Db 7 TTCCACACGCTTCCCAAC 24

RESULT 11

LOCUS A14539/c 28 bp DNA linear PAT 29-SEP-1994

DEFINITION Group 17 ter hybridization probe for detecting Neisseria strains.

ACCESSION A14539

VERSION A14539.1 GI:640860

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 28)

AUTHORS Rosseau,R. and Van Heuverswijn,H.

TITLE Hybridization probes for detecting neisseria strains

JOURNAL Patent: EP 0337896-A 70 18-OCT-1989;

N.V. INNOGENETICS S.A

FEATURES

source

1..28

Location/Qualifiers

BASE COUNT 6 a 3 c 9 g 10 t

ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 28;

Best Local Similarity 83.3%; Pred. No. 6.3e+04;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 TTCCACACGCTTCCCAAC 19

Db 22 TTCCACACGCTTCCCAAC 5

RESULT 12

LOCUS A14540 28 bp DNA linear PAT 29-SEP-1994

DEFINITION Group 17 quater hybridization probe for detecting Neisseria strains.

ACCESSION A14540

VERSION A14540.1 GI:640861

KEYWORDS

FEATURES

source

1..35

Location/Qualifiers

BASE COUNT 6 a 3 c 9 g 10 t

ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 28;

Best Local Similarity 83.3%; Pred. No. 6.3e+04;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 TTCCACACGCTTCCCAAC 19

Db 22 TTCCACACGCTTCCCAAC 5

SOURCE

ORGANISM

synthetic construct.

synthetic construct

artificial sequences.

REFERENCE

1 (bases 1 to 28)

AUTHORS Rosseau,R. and Van Heuverswijn,H.

TITLE Hybridization probes for detecting neisseria strains

JOURNAL Patent: EP 0337896-A 71 18-OCT-1989;

N.V. INNOGENETICS S.A

FEATURES

source

1..28

Location/Qualifiers

BASE COUNT 6 a 3 c 9 g 10 t

ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 28;

Best Local Similarity 83.3%; Pred. No. 6.3e+04;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 TTCCACACGCTTCCCAAC 19

Db 22 TTCCACACGCTTCCCAAC 5

RESULT 13

LOCUS AX248913 31 bp DNA linear PAT 28-SEP-2001

DEFINITION Sequence 992 from patent WO0166800.

ACCESSION AX248913

VERSION AX248913.1 GI:15863536

KEYWORDS

SOURCE

ORGANISM

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 31)

AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.

TITLE Human single nucleotide polymorphisms

JOURNAL Patent: WO 0166800-A 992 13-SEP-2001;

WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)

FEATURES

source

1..31

Location/Qualifiers

BASE COUNT 2 a 14 c 7 g 7 t 1 others

ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 31;

Best Local Similarity 75.0%; Pred. No. 6.2e+04;

Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 GTTCCGACGCTTGCACCT 20

Db 10 GTTCCGACGCTTGCACCT 29

RESULT 14

LOCUS AR212154 35 bp DNA linear PAT 20-JUN-2002

DEFINITION Sequence 21 from patent US 6399571.

ACCESSION AR212154

VERSION AR212154.1 GI:21515663

KEYWORDS

SOURCE

ORGANISM

unknown.

Unclassified.

REFERENCE

1 (bases 1 to 35)

AUTHORS Gray,P.W. and Tjoeiker,L.W.

TITLE Chitinase chitin-binding fragments

JOURNAL Patent: US 6399571-A 21 04-JUN-2002;

FEATURES

source

1..35

Location/Qualifiers

BASE COUNT 2 a 14 c 7 g 7 t 1 others

ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 31;

Best Local Similarity 75.0%; Pred. No. 6.2e+04;

Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 GTTCCGACGCTTGCACCT 20

Db 10 GTTCCGACGCTTGCACCT 29

BASE COUNT 13 a 8 c 6 g 8 t
ORIGIN

Query Match 65.0%; Score 13; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 7.9e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTCCGAGCCTTG 14
|||||
Db 8 TTCCGAGCCTTG 20

RESULT 15

AX370542

LOCUS AX370542 24 bp DNA linear PAT 16-FEB-2002

DEFINITION Sequence 61 from Patent WO0196371.

ACCESSION AX370542

VERSION AX370542.1 GI:18857578

KEYWORDS

SOURCE synthetic construct.

ORGANISM synthetic construct.

REFERENCE 1. artificial sequences.

AUTHORS Broenner,G., Ciossek,T., Dohrmann,C., Haeder,T. and Rothe,M.

TITLE Adipose-related gene

JOURNAL Patent: WO 0196371-A 61 20-DEC-2001;

DEVELOPER AG (DE)

FEATURES Location/Qualifiers

1..24
source /organism="synthetic construct"

BASE COUNT 7 a 9 c 6 g 2 t

ORIGIN

Query Match 64.0%; Score 12.8; DB 6; Length 24;
Best Local Similarity 87.5%; Pred. No. 1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCCGAGCCTTGCC 16
|||||
Db 3 GTTCCGAGCAGGCC 18

Search completed: November 28, 2002, 18:20:36
Job time : 1164.07 secs

Plate: 0451 row: N column: 02
Seq primer: CGTCTTAAACGACGCCAGT
Class: Plasmid ends
High quality sequence stop: 41.
Location/Qualifiers

FEATURES
source

1..41
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U08C1M0451N02"
/clone_lib="Mouse 10kb plasmid U08C1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1147321419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 8 a 20 c 8 g 5 t
ORIGIN

Query Match 69.58; Score 13.2; DB 17; Length 41;
Best Local Similarity 83.3%; Pred. No. 5.5e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GCGCTGCAGCGCGATG 18
||||| ||||| ||||| |||||
DB 20 GCGCTGCAGCGCGCTGC 3

RESULT 2
A1036497/c 43 bp mRNA linear EST 26-JUN-1998
LOCUS ubd55q12.R1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone
DEFINITION IMAGE:1382662.5; similar to SW:EMP2_HUMAN P54851 EPTTHRLAL
MEMBRANE PROTEIN-2; mRNA sequence.
ACCESSION A1036497
VERSION A1036497.1 GI:3260188
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 43)
REFERENCE
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubucque,T.,
Geisell,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Stepcoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,C., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HIMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HIMI Mouse EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mousest@wustl.wustl.edu
This clone is available royalty-free through INL; contact the

TITLE
JOURNAL
COMMENT

IMAGE Consortium (info@image.llnl.gov) for further information.
M01:905130
Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers

FEATURES
source

1..43
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:1382662"
/clone_lib="Soares_mammary_gland_NMLMG"
/sex="Female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
/note="Vector: pRT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 7 a 20 c 12 g 4 t
ORIGIN

Query Match 69.58; Score 13.2; DB 9; Length 43;
Best Local Similarity 83.3%; Pred. No. 5.6e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GGTCTGCAGCGCGATGCT 19
||||| ||||| ||||| |||||
DB 26 GGTCTGCAGCGCGATGCT 9

RESULT 3
A107642/c 50 bp mRNA linear EST 30-AUG-2001
LOCUS A107642 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION LNC11936, mRNA sequence.
ACCESSION A107642
VERSION A107642.1 GI:13557163
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
REFERENCE
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
Contact: Yutaka Suzuki
Department of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source

1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="LNC11936"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfluminate treated U937 cells"

BASE COUNT 8 a 20 c 10 g 12 t
ORIGIN

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Query Match      69.5%; Score 13.2; DB 9; Length 50;
Best Local Similarity 83.3%; Pred. No. 5.7e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGCTCGACGCGGATGG 18
    ||| ||||| ||||| ||
Db 45 GGGACTGCATCGGGAAG 28

RESULT 4
AUI07643/c 50 bp mRNA linear EST 30-AUG-2001
LOCUS AUI07643 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION ZR66C769, mRNA sequence.
ACCESSION AUI07643
VERSION AUI07643.1 GI:13557164
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Tsaira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL MEDLINE
CONTACT Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
source
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ZR66C769"
/note="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfluminate treated U937 cells"
BASE COUNT 9 a 21 c 10 g 10 t
ORIGIN
Query Match      69.5%; Score 13.2; DB 9; Length 50;
Best Local Similarity 83.3%; Pred. No. 5.7e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGCTCGACGCGGATGG 18
    ||| ||||| ||||| ||
Db 42 GGGACTGCATCGGGAAG 25

RESULT 5
A2834659/c 43 bp DNA linear GSS 20-FEB-2001
LOCUS A2834659 Mouse 10kb plasmid UUCGM library Mus musculus genomic
clone UUCGM117B01 R, DNA sequence.
ACCESSION A2834659
VERSION A2834659.1 GI:13004567
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 43)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beccorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellily

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TITLE
JOURNAL
COMMENT
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0117 row: B column: 01
Seq primer: CACGACGAGAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 43.
Location/Qualifiers
1..43
/organism="Mus musculus"
/strain="C57Bl/6J"
/db_xref="taxon:10090"
/clone="UUCGM117B01"
/clone_lib="Mouse 10kb plasmid UUCGM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-
/note="Vector: PMD42uv; Purified genomic DNA from M.
musculus C57Bl/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/)
The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1147321141gb1AF129072.1), a copy-number
inducible derivative of Plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT 7 a 17 c 6 g 13 t
ORIGIN

```

```

Query Match      66.3%; Score 12.6; DB 17; Length 43;
Best Local Similarity 78.9%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGCTCGACGCGGATGCT 19
    | | | | | | | | | | | |
Db 22 GAGGCTCGACGCGGATGCT 4

RESULT 6
AUI05954/c 50 bp mRNA linear EST 30-AUG-2001
LOCUS AUI05954 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION INEB0085, mRNA sequence.
ACCESSION AUI05954
VERSION AUI05954.1 GI:1355475
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Tsaira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki

```

TITLE
Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL
EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE
21270072
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshimoto-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
, S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
source
1. 50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="1NEB0085"
/clone_1lb="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylsulfoxide treated u937 cells"
BASE COUNT
12 a 10 c 18 g 10 t
ORIGIN
Query Match 65.3%; Score 12.4; DB 9; Length 50;
Best Local Similarity 92.9%; Pred. No. 1.3e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 3 GGTCTGCAGCGCGAT 16
|||||||
DB 33 CTCCTCAGCGCGAT 46
RESULT 7
BE736376 38 bp mRNA linear EST 15-SEP-2000
LOCUS
60130651.F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640802 5',
DEFINITION
mRNA sequence.
ACCESSION
BE736376
VERSION
BE736376.1 GI:10150368
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 38)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapds@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LHC345 row: j column: 03
High quality sequence stop: 38.
FEATURES
source
1. 38
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3640802"
/clone_1lb="NIH_MGC_39"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site: 1; XhoI;
Site: 2; EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin

(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies).
BASE COUNT
9 a 6 c 19 g 4 t
ORIGIN
Query Match 64.2%; Score 12.2; DB 12; Length 38;
Best Local Similarity 82.4%; Pred. No. 1.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 GGTCTGCAGCGCGATG 17
|||||||
DB 7 GGGCTGCAGCTGCAGG 23
RESULT 8
B1665248 39 bp mRNA linear EST 12-SEP-2001
LOCUS
60328895.F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5323189 5',
DEFINITION
mRNA sequence.
ACCESSION
B1665248
VERSION
B1665248.1 GI:15579481
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 39)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapds@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LHAM1819 row: m column: 14
High quality sequence stop: 39.
FEATURES
source
1. 39
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5323189"
/clone_1lb="NCI CGAP Mam6"
/sex="female; virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-Sport6; Site: 1; SalI;
Site: 2; NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT
8 a 9 c 13 g 9 t
ORIGIN
Query Match 64.2%; Score 12.2; DB 13; Length 39;
Best Local Similarity 82.4%; Pred. No. 1.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 2 GGTCTGCAGCGCGATGC 18
|||||||
DB 19 GTTCTGCAGCTGCAGAC 35
RESULT 9
BF788284 39 bp mRNA linear EST 12-JAN-2001
LOCUS
60211401.F1 NCI_CGAP_K1d14 Mus musculus cDNA clone IMAGE:4241957
DEFINITION

ACCESSION	5', mRNA sequence.
VERSION	BF788284
KEYWORDS	BF788284.1 GI:12093320
SOURCE	EST.
ORGANISM	house mouse.
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL	1 (bases 1 to 39)
COMMENT	NIH-MGC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strassberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLN859 row: b column: 06 High quality sequence stop: 39. Location/Qualifiers 1..39 /organism="Mus musculus" /strain="FVB/N" /db_xref="taxon:10090" /clone="IMAGE:4241957" /clone_lib="NCLCGAP.K1d14" /lab_host="DH10B (TI phage-resistant)" /note="Organ: Kidney; Vector: pCMW-SPOrt6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCLCGAP Library. " 7 a 10 c 15 g 7 t
BASE COUNT	
ORIGIN	
Query Match	63.2%; Score 12; DB 12; Length 39;
Best Local Similarity	100.0%; Pred. NO. 1.8e+05;
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	6 TGCACGCCGATG 17
Db	9 TGCACGCCGATG 20
RESULT 10	
LOCUS	A1197706/c 43 bp mRNA linear EST 14-OCT-1998
DEFINITION	uc48612.r1 Soares mammary.gland NMLMG Mus musculus cDNA clone IMAGE:149482 5' similar to TR:016786 O16786 T21D12.3 PROTEIN. ;
ACCESSION	A1197706
VERSION	A1197706.1 GI:3750312
KEYWORDS	EST.
ORGANISM	house mouse.
SOURCE	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE	1 (bases 1 to 43)
JOURNAL	Maria M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
COMMENT	Seisler, S., Kudaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, R., Steptoe, M., Tan, F., Underwood, R., Moore, B., Thelsting, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R. The Mashu-HMT Mouse EST Project Unpublished (1996) Contact: Maria M/Mouse EST Project Washu-HMT Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800

Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the IMAG Consortium (infoimage.lnl.gov) for further information.
MGI:931986
Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
Seq primer: -28m13 rev2 Err from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..43
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:1494382"
/clone_lib="Soares_mammary_gland_NMLMG"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT
ORIGIN
5 a 14 c 16 g 8 t

Query Match 63.2%; Score 12; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGCTGTCACGC 12
|||||
db 26 GGGCTGTCACGC 15

RESULT 11
AUI07049/c 50 bp mRNA linear EST 30-AUG-2001
LOCUS AUI07049 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION KAT03213, mRNA sequence.
ACCESSION AUI07049
VERSION AUI07049.1 GI:13556570
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki.Y., Taira.H., Tanoda.T., Mizushima-Sugano.J., Sese.J., Hatachi.H., Ota.T., Isogai.T., Tanaka.T., Morishita.S., Okubo.K., Sakaki.Y., Nakamura.Y., Suyama.A. and Sugano.S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki.Y., Yoshitomo-Nakagawa.K., Maruyama.K., Suyama.A. and Sugano.S.
5' Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="KAT03213"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and

BASE COUNT 9 a 14 c 22 g 5 t
 dimethylfumurate treated u937 cells*

Query Match 63.2%; Score 12; DB 9; Length 50;
 Best Local Similarity 100.0%; Pred. No. 1.9e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 GGGCTGCACGC 12
 11
 Db 49 GGGCTGCACGC 38

RESULT 12
 A1188328 46 bp mRNA linear EST 28-OCT-1998
 LOCUS
 DEFINITION q113c07.x1 Soares Placenta, 8to9weeks-2Nbhp8lc9w Homo sapiens cDNA
 clone IMAGE:1723536.3 similar to SW:G45.CRI10 P24523 GROWTH
 ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD45. ; mRNA sequence.
 A1188328
 VERSION A1188328.1 GI:3739537
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 46)
 NC1-GAP http://www.ncbi.nlm.nih.gov/nc1gap.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strussberg, Ph.D.
 Email: sgabs-remail.nih.gov
 This clone is available royalty-free through LNL: contact the
 IMAGE Consortium (InfoImage.lnl.gov) for further information.
 Trace considered overall poor quality
 Insert Length: 1083 Std Error: 0.00
 Seq primer: -40UP from G1bco
 High quality sequence stop: 1.
 Location/Qualifiers
 1. 46
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="1723536"
 /clone_lib="Soares_placenta_8to9weeks-2Nbhp8lc9w"
 /dev_stage="two placenta; one from 8 weeks and another
 from 9 weeks post conception"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: placenta; Vector: p773D (Pharmacia) with a
 modified polylinker. Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TCTTACCAATCTGAGTGGAGCGCGCGCATTTTCTTTTCTTTTCTTTT 3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified p773 vector
 (Pharmacia). Library constructed by Bento Soares and
 M.Felima Bonaldo."

BASE COUNT 13 a 10 c 14 g 9 t

Query Match 62.1%; Score 11.8; DB 9; Length 46;
 Best Local Similarity 86.7%; Pred. No. 2.3e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 1 GGGCTGCACGC 15
 11
 Db 31 GGGCTGCACGC 45

RESULT 13
 A0026239 48 bp DNA linear GSS 30-JUN-1998
 LOCUS
 DEFINITION 1(3)1170 Drosophila melanogaster P lethal line Drosophila

ACCESSION A0026239
 VERSION A0026239.1 GI:3266524
 KEYWORDS GSS
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 48)
 Spreading, A.C., Stern, D., Beaton, A., Rehm, E.J., Laverly, T., Mozen
 N., Miera, S. and Rubin, G.M.
 TITLE The BDCP gene disruption project: Single P element insertions
 mutating 30% of Drosophila autosomal genes
 JOURNAL Unpublished (1998)
 COMMENT Contact: Gerald Rubin
 Berkeley Drosophila Genome Project
 University of California, Berkeley
 LSA Building, Berkeley, CA 94720-3200, USA
 FAX: 5106439947
 Email: gerry@fruitfly.berkeley.edu
 Sequence recovery method was Inverse PCR.
 Sequence orientation is forward strand relative to 5' end of P
 element

FEATURES
 source
 1. 48
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_lib="Drosophila melanogaster P lethal line"
 /note="Inverse PCR was performed on Drosophila
 melanogaster strains each of which contains a single P
 transposable element insertion that is thought to cause
 either lethality or sterility. The resultant fragment for
 each strain was directly sequenced to determine the
 genomic sequence at the site of insertion. Details of the
 protocols used can be found at
 http://fruitfly.berkeley.edu/P-disrupt/Inverse_pcr.html."

BASE COUNT 15 a 13 c 18 g 2 t

Query Match 62.1%; Score 11.8; DB 17; Length 48;
 Best Local Similarity 86.7%; Pred. No. 2.3e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 5 CTCGACCGGCGATGCT 19
 11
 Db 48 CTCGACCGGCGATGCT 34

RESULT 14
 AUI07919/c 50 bp mRNA linear EST 30-AUG-2001
 LOCUS
 DEFINITION AUI07919 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 ZRV61844, mRNA sequence.
 AUI07919
 ACCESSION AUI07919.1 GI:13557441
 VERSION AUI07919.1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 50)
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
 H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
 Y., Nakamura, Y., Suyama, A. and Sugano, S.
 TITLE Diverse transcriptional initiation revealed by fine, large-scale

JOURNAL
EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE
21270072
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshimoto-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length cDNA library enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
SOURCE
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ZRV61844"
/clone_1id="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"

BASE COUNT
ORIGIN
9 a 11 c 8 g 22 t

Query Match
Best Local Similarity 62.1% Score 11.6; DB 9; Length 50;
Matches 13: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCTGCAGCGGATGG 18
||||| 11 11
Db 20 TCTGCAGCTGGAGCG 6

RESULT 15
TA223G120/c 21 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 223g12, reverse sequence,
genomic survey sequence.
ACCESSION
AL480787
VERSION
AL480787.1 GI:11846556
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei.
ORGANISM
Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

REFERENCE
AUTHORS
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE
JOURNAL
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREP927/4 cutat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES
SOURCE
1..21
Location/Qualifiers

/organism="Trypanosoma brucei"
/strain="TREP927"
/db_xref="taxon:5691"
/clone="223g12"

BASE COUNT
ORIGIN
5 a 8 c 5 g 3 t

Query Match
Best Local Similarity 61.1% Score 11.6; DB 17; Length 21;
Matches 14: Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTCTGCAGCGGATGTT 19
||||| 11 11 11 11 11
Db 21 GGTATGCTGCGGATGTT 4

Search completed: November 28, 2002, 19:30:44
Job time : 1375.59 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 28, 2002, 17:15:39 ; Search time 39.9655 Seconds
(without alignments)
183,088 Million cell updates/sec

Title: US-09-719-737-9

Perfect score: 19

Sequence: 1 ggcgtcgcagcgagatgct 19

Scoring table: IDENTITY-NUC

Gapop 10.0, Gapext 1.0

Searched: 341543 seqs, 19255720 residues

Total number of hits satisfying chosen parameters: 177872

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications, NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	74.7	20	10	US-09-733-294A-63
2	13.2	69.5	38	10	US-09-349-954A-13
3	13.2	69.5	38	10	US-09-907-007-13
4	12.6	66.3	30	10	US-09-730-716-11
5	12.6	66.3	35	9	US-09-826-025-6
6	12.6	66.3	38	10	US-09-850-165-61
7	12.6	66.3	41	9	US-09-925-664-66
8	12.6	66.3	43	10	US-09-766-378A-2
9	12.6	66.3	44	10	US-09-848-164-40
10	12.2	64.2	21	10	US-09-838-785-8
11	12.2	64.2	31	10	US-09-801-274-1241
12	12.2	64.2	31	10	US-09-801-274-1005
13	12.2	64.2	31	10	US-09-801-274-1006
14	11.8	62.1	20	8	US-08-591-486B-100
15	11.8	62.1	20	10	US-09-752-639-110
16	11.8	62.1	20	10	US-09-984-198-110
17	11.6	61.1	26	10	US-09-872-761-9
18	11.6	61.1	20	10	US-09-838-785-17
19	11.6	61.1	45	10	US-09-850-165-24

20	11.4	60.0	16	12	US-10-007-628-13	Sequence 13, Appl
21	11.4	60.0	29	10	US-09-729-674-250	Sequence 250, App
22	11.2	58.9	29	10	US-09-727-198-3	Sequence 3, Appl1
23	11.2	58.9	24	10	US-09-947-770-34	Sequence 34, Appl
24	11.2	58.9	30	9	US-09-252-150-58	Sequence 58, Appl
25	11.2	58.9	31	10	US-09-801-274-1098	Sequence 1098, Ap
26	11.2	58.9	31	10	US-09-801-274-1217	Sequence 1217, Ap
27	11.2	58.9	36	10	US-09-896-853-34	Sequence 34, Appl
28	11.2	58.9	36	12	US-10-020-139-7	Sequence 7, Appl
29	11.2	58.9	39	9	US-09-430-029-12	Sequence 12, Appl
30	11.2	58.9	40	9	US-10-113-246-3	Sequence 3, Appl1
31	11.2	58.9	40	9	US-10-113-238-3	Sequence 3, Appl1
32	11.2	58.9	40	10	US-09-896-853-32	Sequence 32, Appl
33	11.2	58.9	40	10	US-09-865-807-40	Sequence 40, Appl
34	11.2	58.9	40	10	US-09-944-604-7	Sequence 7, Appl1
35	11.2	58.9	40	10	US-09-757-207-2	Sequence 2, Appl1
36	11.2	58.9	40	10	US-09-757-207-5	Sequence 5, Appl1
37	11.2	58.9	40	10	US-09-757-207-6	Sequence 6, Appl1
38	11.2	58.9	41	10	US-09-757-207-1	Sequence 1, Appl1
39	11.2	58.9	41	10	US-09-757-207-7	Sequence 7, Appl1
40	11.2	58.9	42	10	US-09-778-175-12	Sequence 12, Appl
41	11.2	58.9	42	10	US-09-778-175-12	Sequence 12, Appl
42	11.2	58.9	42	10	US-09-335-218-12	Sequence 12, Appl
43	11.2	58.9	44	10	US-09-778-175-6	Sequence 6, Appl1
44	11.2	58.9	44	10	US-09-778-175-6	Sequence 6, Appl1
45	11.2	58.9	44	10	US-09-335-218-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-09-733-294A-63
; Sequence 63, Application US/09733294A
; Patent No. US20020045588A1
GENERAL INFORMATION:
; APPLICANT: Brett P. Montia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freiler
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0527
; CURRENT APPLICATION NUMBER: US/09/733,294A
; PRIOR APPLICATION NUMBER: 2000-12-07
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-733-294A-63
Query Match 74.7%; Score 14.2; DB 10; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0;
Gaps 0;
OY 1 GGGTTCGACGGGATGCT 19
||||| 111111111
DB 1 GGGTTCGACCTGGATGCT 19
RESULT 2
US-09-349-954A-13
; Sequence 13, Application US/09349954A
; Patent No. US20020019027A1
GENERAL INFORMATION:
; APPLICANT: Hayward, Nicholas K.
; APPLICANT: Weber, Gunther
; APPLICANT: Grimmond, Sean
; APPLICANT: No. US20020019027A1denskjold, Magnus


```
RESULT 6
US-09-850-165-61/c
; Sequence 61, Application US/09850165
; Patent No. US20020150580A1
; GENERAL INFORMATION:
; APPLICANT: NEMMAN, ROLAND A.
; APPLICANT: HANNA, NABIL
; APPLICANT: RAAB, RONALD W.
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
; FILE REFERENCE: 037003-0280614
; CURRENT APPLICATION NUMBER: US/09/850,165
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: 09/082,472
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: 08/476,237
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/397,072
; PRIOR FILING DATE: 1995-04-17
; PRIOR APPLICATION NUMBER: 07/912,292
; PRIOR FILING DATE: 1992-07-10
; PRIOR APPLICATION NUMBER: 07/856,281
; PRIOR FILING DATE: 1992-03-23
; PRIOR APPLICATION NUMBER: 07/735,064
; PRIOR FILING DATE: 1991-07-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 61
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-850-165-61

Query Match      66.3%; Score 12.6; DB 10; Length 38;
Best Local Similarity 78.9%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGTCGACGCGGATGCT 19
    |||||
DB 33 GGGTCGACACCATGCT 15

RESULT 7
US-09-925-664-66/c
; Sequence 66, Application US/09925664
; Patent No. US2002016006A1
; GENERAL INFORMATION:
; APPLICANT: Denney, Jr., Dan W.
; TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia
; FILE REFERENCE: GENTOPE-06499
; CURRENT APPLICATION NUMBER: US/09/925,664
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/370,453
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: 08/644,664
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/761,277
; PRIOR FILING DATE: 1996-12-06
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patentln Version 3.1
; SEQ ID NO 66
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-925-664-66

Query Match      66.3%; Score 12.6; DB 9; Length 41;
Best Local Similarity 78.9%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 1 GGGTCGACGCGGATGCT 19
    |||||
DB 37 GGGTCGACACCATGCT 19

RESULT 8
US-09-766-378A-2/c
; Sequence 2, Application US/09766378A
; Patent No. US2002091079A1
; GENERAL INFORMATION:
; APPLICANT: Rhode, Peter R.
; APPLICANT: Acevedo, Jorge
; APPLICANT: Burkhardt, Martin
; APPLICANT: Jiao, Jin-an
; APPLICANT: Wong, Hing C.
; TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, Bronstein, Roberts & Cushman, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: usa
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/766,378A
; FILING DATE: 19-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/960,190
; FILING DATE: 29-Oct-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Corless, Peter F.
; REGISTRATION NUMBER: 33,860
; REFERENCE/DOCKET NUMBER: 48002-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-766-378A-2

Query Match      66.3%; Score 12.6; DB 10; Length 43;
Best Local Similarity 78.9%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGTCGACGCGGATGCT 19
    |||||
DB 38 GGATCTGCAGGCCATGCT 20

RESULT 9
US-09-848-164-40/c
; Sequence 40, Application US/09848164
; Patent No. US20020034513A1
; GENERAL INFORMATION:
; APPLICANT: Rhode, Peter R.
; APPLICANT: Jiao, Jin-an
; APPLICANT: Burkhardt, Martin
; APPLICANT: Wong, Hing
; TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
```

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1 NUMBER OF SEQUENCES: 124
2 CORRESPONDENCE ADDRESS:
3 ADDRESSEE: Dade International, Inc.
4 STREET: 1717 Deerfield Road
5 CITY: Deerfield
6 STATE: Illinois
7 COUNTRY: USA
8 ZIP: 60015
9
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: floppy disk
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: PatentIn Release #1.0, Version #1.30
15
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/09/848,164
18 FILING DATE: 03-May-2001
19 CLASSIFICATION: <Unknown>
20
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: 09/067,615
23 FILING DATE: <Unknown>
24 APPLICATION NUMBER: US 08/382,454
25 FILING DATE: 01-FEB-1995
26 APPLICATION NUMBER: US 08/283,302
27 FILING DATE: 29-JUL-1994
28
29 ATTORNEY/AGENT INFORMATION:
30 NAME: Pearson, Louise S.
31 REGISTRATION NUMBER: 32,369
32 REFERENCE/DOCKET NUMBER: STR-4665-CIP2
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: (708) 267-5300
35 TELEFAX: (708) 267-5376
36
37 INFORMATION FOR SEQ ID NO: 40:
38
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 44 base pairs
41 TYPE: nucleic acid
42 STRANDEDNESS: unknown
43 TOPOLOGY: unknown
44
45 SEQUENCE DESCRIPTION: SEQ ID NO: 40:
46
47 US-09-848-164-40
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: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-838-785-B

Query Match          64.2%; Score 12.2; DB 10; Length 21;
Best Local Similarity 82.4%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GGTCTGCAGCGCATG 18
      1 | 11111 11111
Db      17 GCTGTGCAGCGCATG 1

RESULT 11
US-09-801-274-1241/C
: Sequence 1241, Application US/09801274
: Patent No. US20020032319A1
: GENERAL INFORMATION:
: APPLICANT: Cargill, Michele
: APPLICANT: Iander, Eric S.
: TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
: FILE REFERENCE: 2825.2009-001
: CURRENT APPLICATION NUMBER: US/09/801.274
: PRIOR FILING DATE: 2001-03-07
: PRIOR APPLICATION NUMBER: US 60/187,510
: PRIOR FILING DATE: 2000-03-07
: PRIOR APPLICATION NUMBER: US 60/206,129
: NUMBER OF SEQ. ID NOS: 1802
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 1241
: LENGTH: 31
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-801-274-1241

Query Match          64.2%; Score 12.2; DB 10; Length 31;
Best Local Similarity 82.4%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GGTCTGCAGCGCATG 18
      11111 11 111 111
Db      25 GGTCTGTAGRGCGCTG 9

RESULT 12
US-09-801-274-1005/C
: Sequence 1005, Application US/09801274
: Patent No. US20020032319A1
: GENERAL INFORMATION:
: APPLICANT: Cargill, Michele
: APPLICANT: Iander, James S.
: APPLICANT: Iander, Eric S.
: TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
: FILE REFERENCE: 2825.2009-001
: CURRENT APPLICATION NUMBER: US/09/801.274
: PRIOR FILING DATE: 2001-03-07
: PRIOR APPLICATION NUMBER: US 60/187,510
: PRIOR FILING DATE: 2000-03-07
: PRIOR APPLICATION NUMBER: US 60/206,129
: PRIOR FILING DATE: 2000-05-22
: NUMBER OF SEQ. ID NOS: 1802
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 1005
: LENGTH: 31
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-801-274-1005

Query Match          63.2%; Score 12; DB 10; Length 31;
Best Local Similarity 85.7%; Pred. No. 3.6e+03;

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Matches 12: Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGTCTGCACGGCGA 15
|||||
Db 28 GGTCTGCACGGCGA 15

RESULT 13

US-09-801-274-1006/C
Sequence 1006, Application US/09801274
Patent No. US20020032319A1
GENERAL INFORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Lander, Eric S.
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 2825.2009-001
CURRENT APPLICATION NUMBER: US/09/801,274
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 60/187,510
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 60/206,129
PRIOR FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 1802
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 1006
LENGTH: 31
TYPE: DNA
ORGANISM: Homo sapiens
US-09-801-274-1006

Query Match
Best local Similarity 85.7%; Score 12; DB 10; Length 31;
Matches 12: Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGTCTGCACGGCGA 15
|||||
Db 21 GGTCTGCACGGCGA 8

RESULT 14

US-08-591-486B-100
Sequence 100, Application US/08591486B
Patent No. US20020037866A1
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Georg F
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Collngen, Wolfgang Bivsch
TITLE OF INVENTION: A Pharmaceutical Composition
TITLE OF INVENTION: Comprising Antisense-Nucleic Acid for Prevention and/or Treatment of Neuronal Injury, Degeneration and Cell Death and for the
TITLE OF INVENTION: Treatment of Neoplasms
NUMBER OF SEQUENCES: 185
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh Street, N.W.
CITY: Washington, D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,486B
FILING DATE: 11-JAN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93111059.7
FILING DATE: 10-JUL-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP94/02218
FILING DATE: 6-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10496/P60122
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-9350
TELEX: RCA 248593 IDRA UR
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-591-486B-100

Query Match
Best local Similarity 86.7%; Score 11.8; DB 8; Length 20;
Matches 13: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 CTGTCACGGGATGAT 19
|||||
Db 2 CTGTCACGGGATGAT 16

RESULT 15

US-09-752-639-110
Sequence 110, Application US/09752639
Patent No. US20020091243A1
GENERAL INFORMATION:
APPLICANT: Gatanaga, T.
APPLICANT: Granger, G.A.
TITLE OF INVENTION: Factors Altering Tumor Necrosis
TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
TITLE OF INVENTION: of Use Thereof
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/752,639
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/10793
FILING DATE:
APPLICATION NUMBER: 09/081,385
FILING DATE:
APPLICATION NUMBER: 08/964,747
FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 60/030,761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wu, Frank
REGISTRATION NUMBER: 41,386
REFERENCE/DOCKET NUMBER: 22000-20577.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-752-639-110

Query Match 62.1%; Score 11.8; DB 10; Length 20;
Best Local Similarity 86.7%; Pred. No. 4.4e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Caps 0;
QY 4 TCTGCAGCGCGATGC 18
DB 4 TCTGCAGCGCGATGC 18

Search completed: November 28, 2002, 19:35:04
Job time : 39.9655 secs

STATE: Florida
COUNTRY: United States of America
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,760B
FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/838,702
FILING DATE: 09-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: PACE, DORAN R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: CNG-100C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-848-760B-6

Query Match 66.3%; Score 12.6; DB 4;
Best Local Similarity 78.9%; Pred. No. 1.4e+03;
Matches 15: Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGCTCGACGCCGATGCT 19
DB 33 GGGCTCGACGCCGATGCT 15

RESULT 3
US-08-478-039-37/c
Sequence 37, Application US/08478039
Patent No. 5681722
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATTHEIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292

FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Rodin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens or Monkey
POSITION IN GENE:
CHROMOSOME/SEGMENT: kappa light chain primer with BglII site
US-08-478-039-37

Query Match 66.3%; Score 12.6; DB 1;
Best Local Similarity 78.9%; Pred. No. 1.4e+03;
Matches 15: Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGCTCGACGCCGATGCT 19
DB 33 GGGCTCGACGCCGATGCT 15

RESULT 4
US-08-476-349A-37/c
Sequence 37, Application US/08476349A
Patent No. 5750105
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATTHEIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens or Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: kappa light chain primer with BglII site
US-08-476-349A-37

Query Match 66.3%; Score 12.6; DB 1; Length 38;
Best Local Similarity 78.9%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 GGGCTGCGACGGGATGCT 19
||||||| 1 |||||
Db 33 GGGCTGCGAACACCATGCT 15

RESULT 5
US-08-803-085-8/c
Sequence 8, Application US/08803085
Patent No. 6011138
GENERAL INFORMATION:
APPLICANT: REF, Mitchell E.
APPLICANT: KLOETZER, William S.
APPLICANT: NAKAMURA, Takehiko
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/803,085
FILING DATE: 20-FEB-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-803-085-8

Query Match 66.3%; Score 12.6; DB 3; Length 38;
Best Local Similarity 78.9%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGGCTGCGACGGGATGCT 19
||||||| 1 |||||
Db 33 GGGCTGCGAACACCATGCT 15

RESULT 6
US-08-523-894-30/c
Sequence 30, Application US/08523894
Patent No. 6136310
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Ref, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
POSITION IN GENOME:
CHROMOSOME/SEGMENT: kappa light chain primer with Bgl II site
US-08-523-894-30

Query Match 66.3%; Score 12.6; DB 3; Length 38;
Best Local Similarity 78.9%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 GGGCTGCGACGGGATGCT 19
||||||| 1 |||||
Db 33 GGGCTGCGAACACCATGCT 15

RESULT 7
US-08-761-277A-66/c
Sequence 66, Application US/08761277A
Patent No. 5972334
GENERAL INFORMATION:

APPLICANT: Denney Jr., Dan W.
 TITLE OF INVENTION: Vaccines for Treatment of Lymphoma And
 TITLE OF INVENTION: Leukemia
 NUMBER OF SEQUENCES: 80
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Medien & Carroll, LLP
 STREET: 220 Montgomery Street, Suite 2200
 CITY: San Francisco
 STATE: California
 COUNTRY: United States Of America
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/761,277A
 FILING DATE: 06-DEC-1996
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/644,664
 FILING DATE: 01-MAY-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: MacKnight, Kamrin T.
 REGISTRATION NUMBER: 38,230
 REFERENCE/DOCKET NUMBER: GENITYPE-02406
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 705-8410
 TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 66:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 41 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-761-277A-66
 Query Match 66.3% Score 12.6; DB 2; Length 41;
 Best Local Similarity 78.9% Pred. No. 1.4e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 GGGCTGCGAGCCGATGCT 19
 ||||||| 1 |||||
 Db 37 GGGCTGCGAGCCGATGCT 19

RESULT 8
 US-08-960-190A-2/c
 Sequence 2, Application US/08960190A
 Patent No. 6232445
 GENERAL INFORMATION:
 APPLICANT: Rhode, Peter R.
 APPLICANT: Acevedo, Jorge
 APPLICANT: Burkhardt, Martin
 APPLICANT: Jiao, jin-an
 APPLICANT: Kong, Ming C.
 TITLE OF INVENTION: SOLUBLE MIC COMPLEXES AND
 TITLE OF INVENTION: METHODS OF USE THEREOF
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dike, Bronsteijn, Roberts & Cushman, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/960,190A
 FILING DATE: 29-OCT-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Cortes, Peter F.
 REGISTRATION NUMBER: 33,860
 REFERENCE/DOCKET NUMBER: 48002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 TELEX:
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 43 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-960-190A-2
 Query Match 66.3% Score 12.6; DB 4; Length 43;
 Best Local Similarity 78.9% Pred. No. 1.4e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 GGGCTGCGAGCCGATGCT 19
 ||||||| 1 |||||
 Db 38 GATCTGCGAGCCGATGCT 20

RESULT 9
 US-09-042-353-399/c
 Sequence 399, Application US/09042353
 Patent No. 6255458
 GENERAL INFORMATION:
 APPLICANT: Lonberg, Nils
 APPLICANT: Kay, Robert M.
 TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
 TITLE OF INVENTION: Producing Heterologous Antibodies
 NUMBER OF SEQUENCES: 421
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/042,353
 FILING DATE: 13-MAR-1998
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/810,279
 FILING DATE: 17-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/853,408
 FILING DATE: 18-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/904,068
 FILING DATE: 23-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/990,860
 FILING DATE: 16-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/053,131
 FILING DATE: 26-APR-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 399:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-042-353-399

Query Match 66.3%; Score 12.6; DB 4; Length 43;
Best Local Similarity 78.9%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGCTGCAGCGGATGCT 19
||||| || || || ||
DB 22 GGGCTGCAGCGGATGCT 4

RESULT 10
US-08-758-417A-249/C
Sequence 249 Application US/08758417A
Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California

COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-DEC-1996
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serfatini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 249:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 249:
US-08-758-417A-249

Query Match 66.3%; Score 12.6; DB 4; Length 43;
Best Local Similarity 78.9%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGCTGCAGCGGATGCT 19
||||| || || || ||
DB 22 GGGCTGCAGCGGATGCT 4

RESULT 11
US-08-596-387B-40/C
Sequence 40 Application US/08596387B
Patent No. 5869270
GENERAL INFORMATION:
APPLICANT: Rhode, Peter R.
APPLICANT: Jiao, Jin-An
APPLICANT: Burkhardt, Martin
APPLICANT: Wong, Hing
TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Jade International, Inc.
STREET: 1717 Deerfield Road
CITY: Deerfield

STATE: Illinois
COUNTRY: USA
ZIP: 60015
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/596.387B
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09816
FILING DATE: 31-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/382,454
FILING DATE: 01-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,302
FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Pearson, Louise S.
REGISTRATION NUMBER: 32,369
REFERENCE/DOCKET NUMBER: STR-4665-CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 267-5300
TELEFAX: (708) 267-5376
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
US-08-596-387B-40

APPLICATION NUMBER: 08/596,387
 FILING DATE:
 PRIOR APPLICATION DATA: US 08/382,454
 APPLICATION NUMBER: US 08/382,454
 FILING DATE: 01-FEB-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/283,302
 FILING DATE: 29-JUL-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Pearson, Louise S.
 REGISTRATION NUMBER: 32,569
 REFERENCE/DOCKET NUMBER: STR-4665-CIP22
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (708) 267-5370
 TELEFAX: (708) 267-5376
 INFORMATION FOR SEQ ID NO: 40:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 44 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown

TELEFAX: (708) 267-5376
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
PCT-US95-09816A-40

Query Match
Best Local Similarity 66.3%; Score 12.6; DB 5; Length 44;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGCTCTGCAGCGGATGCT 19
DB 39 GGATCTGCAGAGCCATGCT 21

RESULT 14
US-08-332-766A-78
Sequence 78, Application US/08332766A
Patent No. 5843647
GENERAL INFORMATION:
APPLICANT: JEFFREYS, Alec J.
APPLICANT: ARMOUR, John
TITLE OF INVENTION: SIMPLE TANDEM REPEATS
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DABRY & CUSHMAN, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,766A
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9326052.9
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BIRD, Donald J.
REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 217211/M94/0434/GB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-332-766A-78

Query Match
Best Local Similarity 65.3%; Score 12.4; DB 2; Length 20;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 GGCTGCAGCGGAT 16
DB 2 GACTGCAGCGGAT 15

RESULT 15

US-09-418-640-56
Sequence 56, Application US/09418640
Patent No. 6140125
GENERAL INFORMATION:
APPLICANT: Jennifer K. Taylor
APPLICANT: Lex M. Cosert
TITLE OF INVENTION: ANTISENSE MODULATION OF BCL-6 EXPRESSION
FILE REFERENCE: R1S-0102
CURRENT APPLICATION NUMBER: US/09/418,640
CURRENT FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 56
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: Antisense Oligonucleotide
US-09-418-640-56

Query Match
Best Local Similarity 65.3%; Score 12.4; DB 3; Length 20;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGCTCTGCAGCGG 14
DB 7 GGCTCTGCAGCGTG 20

Search completed: November 28, 2002, 19:32:50
Job time : 39.3376 secs

1

PT macrophage colony stimulating factor receptors, used for treating or
PT preventing asthma, allergies, hypereosinophilia, inflammation or cancer
XX
XX
PS Claim 5; Page 23; 72pp; English.
XX
XX This is an antisense oligonucleotide directed against the common beta
CC subunit of the interleukin-3 (IL-3) receptor, the interleukin-5 (IL-5)
CC receptor and the granulocyte macrophage colony stimulating factor
CC (GM-CSF) receptor. The antisense oligonucleotide inhibits IL-3, IL-5
CC and GM-CSF receptor expression. IL-3, IL-5 and GM-CSF are cytokines
CC involved in eosinophil proliferation and survival, they are increased in
CC asthma and atopic diseases, and are also involved in the indefinite
CC proliferation of certain neoplastic diseases. The invention relates to
CC antisense oligonucleotides directed against a nucleic acid sequence
CC encoding either a chemokine receptor (CCR3), a common subunit of
CC interleukin-4 (IL-4) and interleukin-13 (IL-13) receptors, or a common
CC subunit of IL-3, IL-5 and GM-CSF receptors. The antisense
CC oligonucleotides can be used in the treatment or prevention of asthma,
CC allergy, hypereosinophilia, general inflammation or cancer.
XX
SQ Sequence 19 BP; 2 A; 3 C; 10 G; 4 T; 0 other;
Query Match 100.0%; Score 19; DB 21; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCGTCTGCACGGCGATGCT 19
|||||
DB 1 GCGTCTGCACGGCGATGCT 19
RESULT 2
AA256194
ID AA256194 standard; DNA; 19 BP.
XX
AC AA256194;
XX
XX 28-MAR-2000 (first entry)
XX
XX Oligonucleotide 106 for IL-3/IL-5/GM-CSF receptor expression inhibition.
XX
XX Interleukin-3; IL-3; interleukin-5; IL-5; antisense oligonucleotide;
KW asthma; allergy; cancer; receptor expression inhibitor; cytokine;
KW inflammation; hypereosinophilia; eosinophil proliferation;
KW granulocyte macrophage colony stimulating factor; GM-CSF; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9966037-A2.
PN
XX
XX 23-DEC-1999.
PD
XX
XX 17-JUN-1999; 99MO-CA00572.
PF
XX
XX 17-JUN-1998; 98CA-2235420.
PR
XX
XX (REEX-) RECH EXPERTISES & DEV MEDICAUX PARENZ IN.
PA
XX
XX Renzi P;
PI
XX
XX WPI: 2000-097743/08.
DR
XX
XX Antisense oligonucleotides directed to CCR3, interleukin or granulocyte
PT macrophage colony stimulating factor receptors, used for treating or
PT preventing asthma, allergies, hypereosinophilia, inflammation or cancer
XX
XX
XX
PS Claim 5; Page 25; 72pp; English.
XX
XX This is an antisense oligonucleotide directed against the common beta
CC subunit of the interleukin-3 (IL-3) receptor, the interleukin-5 (IL-5)
CC receptor and the granulocyte macrophage colony stimulating factor
CC (GM-CSF) receptor. The antisense oligonucleotide inhibits IL-3, IL-5
CC and GM-CSF receptor expression. IL-3, IL-5 and GM-CSF are cytokines
CC involved in eosinophil proliferation and survival, they are increased in
CC asthma and atopic diseases, and are also involved in the indefinite
CC proliferation of certain neoplastic diseases. The invention relates to
CC antisense oligonucleotides directed against a nucleic acid sequence
CC encoding either a chemokine receptor (CCR3), a common subunit of
CC interleukin-4 (IL-4) and interleukin-13 (IL-13) receptors, or a common
CC subunit of IL-3, IL-5 and GM-CSF receptors. The antisense
CC oligonucleotides can be used in the treatment or prevention of asthma,
CC allergy, hypereosinophilia, general inflammation or cancer.
XX
SQ Sequence 19 BP; 2 A; 3 C; 9 G; 5 T; 0 other;
Query Match 94.7%; Score 18; DB 21; Length 19;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GCGTCTGCACGGCGATGCT 19
|||||
DB 1 GCGTCTGCACGGCGATGCT 18
RESULT 3
AA256195
ID AA256195 standard; DNA; 19 BP.
XX
XX
AC AA256195;
XX
XX 28-MAR-2000 (first entry)
XX
XX Oligonucleotide 108 for IL-3/IL-5/GM-CSF receptor expression inhibition.
XX
XX Interleukin-3; IL-3; interleukin-5; IL-5; antisense oligonucleotide;
KW asthma; allergy; cancer; receptor expression inhibitor; cytokine;
KW inflammation; hypereosinophilia; eosinophil proliferation;
KW granulocyte macrophage colony stimulating factor; GM-CSF; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9966037-A2.
PN
XX
XX 23-DEC-1999.
PD
XX
XX 17-JUN-1999; 99MO-CA00572.
PF
XX
XX 17-JUN-1998; 98CA-2235420.
PR
XX
XX (REEX-) RECH EXPERTISES & DEV MEDICAUX PARENZ IN.
PA
XX
XX Renzi P;
PI
XX
XX WPI: 2000-097743/08.
DR
XX
XX Antisense oligonucleotides directed to CCR3, interleukin or granulocyte
PT macrophage colony stimulating factor receptors, used for treating or
PT preventing asthma, allergies, hypereosinophilia, inflammation or cancer
XX
XX
XX
PS Claim 5; Page 25; 72pp; English.
XX
XX This is an antisense oligonucleotide directed against the common beta
CC subunit of the interleukin-3 (IL-3) receptor, the interleukin-5 (IL-5)
CC receptor and the granulocyte macrophage colony stimulating factor
CC (GM-CSF) receptor. The antisense oligonucleotide inhibits IL-3, IL-5
CC and GM-CSF receptor expression. IL-3, IL-5 and GM-CSF are cytokines
CC involved in eosinophil proliferation and survival, they are increased in
CC asthma and atopic diseases, and are also involved in the indefinite
CC proliferation of certain neoplastic diseases. The invention relates to
CC antisense oligonucleotides directed against a nucleic acid sequence
CC encoding either a chemokine receptor (CCR3), a common subunit of
CC interleukin-4 (IL-4) and interleukin-13 (IL-13) receptors, or a common
CC subunit of IL-3, IL-5 and GM-CSF receptors. The antisense

CC (GM-CSF) receptor. The antisense oligonucleotide inhibits IL-3, IL-5
CC and GM-CSF receptor expression. IL-3, IL-5 and GM-CSF are cytokines
CC involved in eosinophil proliferation and survival, they are increased in
CC asthma and atopic diseases, and are also involved in the indefinite
CC proliferation of certain neoplastic diseases. The invention relates to
CC antisense oligonucleotides directed against a nucleic acid sequence
CC encoding either a chemokine receptor (CCR3), a common subunit of
CC interleukin-4 (IL-4) and interleukin-13 (IL-13) receptors, or a common
CC subunit of IL-3, IL-5 and GM-CSF receptors. The antisense
CC oligonucleotides can be used in the treatment or prevention of asthma,
CC allergy, hypereosinophilia, general inflammation or cancer.
XX
SQ Sequence 19 BP; 2 A; 3 C; 9 G; 5 T; 0 other;
Query Match 94.7%; Score 18; DB 21; Length 19;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GCGTCTGCACGGCGATGCT 19
|||||
DB 1 GCGTCTGCACGGCGATGCT 18
RESULT 3
AA256195
ID AA256195 standard; DNA; 19 BP.
XX
XX
AC AA256195;
XX
XX 28-MAR-2000 (first entry)
XX
XX Oligonucleotide 108 for IL-3/IL-5/GM-CSF receptor expression inhibition.
XX
XX Interleukin-3; IL-3; interleukin-5; IL-5; antisense oligonucleotide;
KW asthma; allergy; cancer; receptor expression inhibitor; cytokine;
KW inflammation; hypereosinophilia; eosinophil proliferation;
KW granulocyte macrophage colony stimulating factor; GM-CSF; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9966037-A2.
PN
XX
XX 23-DEC-1999.
PD
XX
XX 17-JUN-1999; 99MO-CA00572.
PF
XX
XX 17-JUN-1998; 98CA-2235420.
PR
XX
XX (REEX-) RECH EXPERTISES & DEV MEDICAUX PARENZ IN.
PA
XX
XX Renzi P;
PI
XX
XX WPI: 2000-097743/08.
DR
XX
XX Antisense oligonucleotides directed to CCR3, interleukin or granulocyte
PT macrophage colony stimulating factor receptors, used for treating or
PT preventing asthma, allergies, hypereosinophilia, inflammation or cancer
XX
XX
XX
PS Claim 5; Page 25; 72pp; English.
XX
XX This is an antisense oligonucleotide directed against the common beta
CC subunit of the interleukin-3 (IL-3) receptor, the interleukin-5 (IL-5)
CC receptor and the granulocyte macrophage colony stimulating factor
CC (GM-CSF) receptor. The antisense oligonucleotide inhibits IL-3, IL-5
CC and GM-CSF receptor expression. IL-3, IL-5 and GM-CSF are cytokines
CC involved in eosinophil proliferation and survival, they are increased in
CC asthma and atopic diseases, and are also involved in the indefinite
CC proliferation of certain neoplastic diseases. The invention relates to
CC antisense oligonucleotides directed against a nucleic acid sequence
CC encoding either a chemokine receptor (CCR3), a common subunit of
CC interleukin-4 (IL-4) and interleukin-13 (IL-13) receptors, or a common
CC subunit of IL-3, IL-5 and GM-CSF receptors. The antisense

CC oligonucleotides can be used in the treatment or prevention of asthma,
 CC allergy, hyperesinophilia, general inflammation or cancer.
 XX
 SQ Sequence 19 BP; 3 A; 3 C; 10 G; 3 T; 0 other;

Query Match 94.7%; Score 18; DB 21; Length 19;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGTCGACGGGATG 18
 |||||
 DB 2 GGGTCGACGGGATG 19

RESULT 4

AAZ56199
 ID AAZ56199 standard; DNA: 19 BP.

AC AAZ56199;

DT 28-MAR-2000 (first entry)

DE Oligonucleotide 105 for IL-3/IL-5/GM-CSF receptor expression inhibition.

KW Interleukin-3; IL-3; interleukin-5; IL-5; antisense oligonucleotide;

KW asthma; allergy; cancer; receptor expression inhibitor; cytokine;

KW inflammation; hyperesinophilia; eosinophil proliferation;

KW granulocyte macrophage colony stimulating factor; GM-CSF; ss.

OS Homo sapiens.

PN WO9966037-A2.

PD 23-DEC-1999.

PE 17-JUN-1999; 99MO-CA00572.

PR 17-JUN-1998; 98CA-2235420.

PA (REEX-) RECH EXPERTISES & DEV MEDICAUX PARENZ IN.

PI Renzi P;

PS WPI: 2000-097743/08.

DR Antisense oligonucleotides directed to CCR3, interleukin or granulocyte

PT macrophage colony stimulating factor receptors, used for treating or

PT preventing asthma, allergies, hyperesinophilia, inflammation or cancer

PT

PT

PT

PT

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PT

PT

PT

PT

PT

PT

OY 3 GTCGACGGGATG 19
 |||||
 DB 1 CTCGACGGGATG 17

Query Match 84.2%; Score 16; DB 21; Length 19;
 Best Local Similarity 100.0%; Pred. No. 23+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGTCGACGGGAT 16
 |||||
 DB 4 GGGTCGACGGGAT 19

RESULT 5

AAZ56196
 ID AAZ56196 standard; DNA: 19 BP.

AC AAZ56196;

DT 28-MAR-2000 (first entry)

DE Oligonucleotide 110 for IL-3/IL-5/GM-CSF receptor expression inhibition.

KW Interleukin-3; IL-3; interleukin-5; IL-5; antisense oligonucleotide;

KW asthma; allergy; cancer; receptor expression inhibitor; cytokine;

KW inflammation; hyperesinophilia; eosinophil proliferation;

KW granulocyte macrophage colony stimulating factor; GM-CSF; ss.

OS Homo sapiens.

PN WO9966037-A2.

PD 23-DEC-1999.

PE 17-JUN-1999; 99MO-CA00572.

PR 17-JUN-1998; 98CA-2235420.

PA (REEX-) RECH EXPERTISES & DEV MEDICAUX PARENZ IN.

PI Renzi P;

PS WPI: 2000-097743/08.

DR Antisense oligonucleotides directed to CCR3, interleukin or granulocyte

PT macrophage colony stimulating factor receptors, used for treating or

PT preventing asthma, allergies, hyperesinophilia, inflammation or cancer

PT

PT

PT

PT

PT

PT

PT

PT

PT

PT

PT

PT

PT

PT

PT

PT

PT

```

AC AAH45301;
XX
XX
DF 10-SEP-2001 (first entry)
XX
XX DE Human Bcl-2 mutagenic primer oligo-4 for S70D substitution.
XX
XX KW Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; primer; ss.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200142459-A1.
XX
XX PD 14-JUN-2001.
XX
XX PF 07-DEC-2000; 2000WO-JP08667.
XX
XX PR 09-DEC-1999; 99JP-0350427.
XX
XX PA (HISM ) HISAMITSU PHARM CO LTD.
XX
XX PI Shibazaki F, Kuma H;
XX DR WPI: 2001-381681/40.
XX
XX PT New Apoptosis Inhibitors, useful for treating apoptosis related
XX disorders -
XX PS Example 1; Page 10; 43pp; Japanese.
XX
XX CC The invention relates to an apoptosis inhibitor comprising the
XX CC amino acid sequence of Bcl-2 protein in which at least one serine
XX CC residue is substituted by alanine or aspartic acid. The protein has
XX CC increased apoptosis inhibitory activity compared with the wild type
XX CC Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment
XX CC of disorders caused by apoptosis. The present sequence was used to
XX CC create a mutant Bcl-2 protein of the invention.
XX
XX SO Sequence 27 BP; 2 A; 8 C; 12 G; 5 T; 0 other;

Query Match 77.9%; Score 14.8; DB 22; Length 27;
Best Local Similarity 88.9%; Pred. No. 8.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Caps 0;

QY 2 GGTCTGCACGCGGATGCT 19
   |||
DB 1 GGTCTGCACGCGGATGCT 18

RESULT 7
AAS96640
ID AAS96640 standard; DNA: 20 BP.
XX
XX AC AAS96640;
XX
XX DT 09-APR-2002 (first entry)
XX
XX DE Telomerase reverse transcriptase, antisense oligonucleotide #50.
XX
XX KW Telomerase reverse transcriptase; TERT; cytosolic; apoptosis;
XX KW cell growth inhibitor; antisense oligonucleotide;
XX KW antisense technology; ss.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO20018198-A1.
XX
XX PD 22-NOV-2001.
XX
XX PR 15-MAY-2001; 2001WO-US15774.
XX
XX PH 16-MAY-2000; 2000US-0572423.

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PR 07-DEC-2000; 2000US-0733294.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX PT Monta BP, Gaarde WA, Freiler SM, Wanciewicz E;
XX
XX DR WPI: 2002-075321/10.
XX
XX PT New compound targeted to nucleic acid molecule encoding telomerase
XX PT transcriptase (TERT), which specifically hybridises with and inhibits
XX PT expression of TERT, useful for modulating apoptosis and inhibiting cell
XX PT growth -
XX
XX PS Example 19; Page 91; 154pp; English.
XX
XX CC The invention describes a compound, 8-50 nucleobases in length targeted
XX CC to a nucleic acid molecule encoding human TERT (telomerase reverse
XX CC transcriptase), where the compound specifically hybridises with and
XX CC inhibits the expression of TERT. A series of oligonucleotides were
XX CC designed to target different regions of the human TERT RNA. These were
XX CC 20 nucleotides in length and composed of a central gap region consisting
XX CC of ten 2'-deoxynucleotides, flanked on both sides (5' and 3' directions)
XX CC by five-nucleotide wings. The wings were composed of 2'-methoxyethyl
XX CC (2'-MOE) nucleotides. The compounds were analysed for their effect on
XX CC human TERT mRNA levels by reverse transcriptase (RT)-polymerase chain
XX CC reaction (PCR). The compound is useful for inhibiting the expression of
XX CC TERT in cells or tissues, for treating a human having disease or
XX CC condition associated with TERT, for modulating apoptosis, for inhibiting
XX CC cell growth (preferably, cancer cell growth), in antisense therapy and
XX CC for diagnostics and therapeutics. This sequence is an antisense
XX CC oligonucleotide used to modulate the activity of nucleic acid molecules
XX CC encoding TERT, described in the method of the invention.
XX
XX SO Sequence 20 BP; 2 A; 5 C; 8 G; 5 T; 0 other;

Query Match 74.7%; Score 14.2; DB 24; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Caps 0;

QY 1 GGGTCTGCACGCGGATGCT 19
   |||||
DB 1 GGGTCTGCACGCGGATGCT 19

RESULT 8
AAA30293/c
ID AAA30293 standard; DNA: 34 BP.
XX
XX AC AAA30293;
XX
XX DT 11-SEP-2000 (first entry)
XX
XX DE R. eutropha toluene monooxygenase tomk primer, tom-K.
XX
XX KW Toluene monooxygenase; carcinogen; halogenated aliphatic hydrocarbon;
XX KW halogenated aromatic hydrocarbon; environmental pollution;
XX KW environmental remediation; enzyme; tomk primer;
XX KW site-directed mutagenesis; ss.
XX
XX OS Ralstonia eutropha strain T864.
XX
XX PN EP106191-A2.
XX
XX PD 07-JUN-2000.
XX
XX PR 03-DEC-1999; 99EP-0124209.
XX
XX PR 03-DEC-1998; 98JP-0344506.
XX
XX PA (CANO ) CANON KK.
XX
XX PT Yano T, Nomoto T, Imamura T;
XX

```


DB 18 CTCGACGGTATGCT 32

RESULT 11

AKT34741
ID AAT34741 standard; DNA: 47 BP.

XX AAT34741;

XX 23-SEP-1996 (first entry)

DE PCR primer OPR141 used in construction of MHC fusion complex vector.

XX MHC; major histocompatibility complex; PCR; polymerase chain reaction;

XX T cell activity; modulator; antagonist; immune disorder; allergy;

XX multiple sclerosis; insulin-dependent diabetes mellitus;

XX rheumatoid arthritis; myasthenia gravis; ss.

XX Synthetic.

XX MO9604314-A1.

XX 15-FEB-1996.

XX 31-JUN-1995; 95WO-US09816.

XX 01-FEB-1995; 95US-0382454.

XX 29-JUL-1994; 94US-0283302.

XX (DADE-) DADE INT INC.

XX Chavallaz P-A, Edwards AC, Grammer S, Jiao J-A, Rhode PR;

XX Weidanz JA, Wong HC;

XX WPI: 1996-129343/13.

XX Major histocompatibility complex fusion complex for modulating T

XX cell activity - used in the treatment of immune disorders, e.g.

XX multiple sclerosis, IDDM and rheumatoid arthritis

XX Example 1, Fig 8: 210pp: English.

XX AAT34735-T34750 are PCR primers used in the construction of MHC fusion

XX complexes capable of modulating T cell activity. The MHC fusion complex

XX comprises a MHC molecule containing a peptide-binding groove and a

XX presenting peptide covalently linked to the MHC molecule and opt. a

XX transmembrane domain. Multivalent MHC fusion complexes may also be

XX made comprising 2 or more linked MHC fusion complexes. DNA encoding

XX a MHC fusion complex may be cloned into a host cell to express the

XX complex. The transformed cells may then be used to identify peptides

XX that modulate, pre-, antagonise, T cell activity. DNA encoding a MHC

XX fusion complex or a single chain fusion molecule may be used to

XX vaccinate a mammal against a targeted disorder. The fusion

XX complexes may be used to suppress an immune response in an animal

XX suffering from an immune disorder e.g. multiple sclerosis, insulin-

XX dependent diabetes mellitus, rheumatoid arthritis, myasthenia

XX gravis or chronic allergies. The complexes may also be used in the

XX treatment of livestock and pets such as cats and dogs. The MHC

XX fusion complexes can be produced such that they contain a single

XX antigenic peptide including one of known structure, additionally a

XX wide range of peptides can be presented for T cell interaction.

XX Sequence 47 BP; 9 A; 11 C; 18 G; 8 T; 1 other;

XX Query Match 70.5%; Score 13.4; DB 17; Length 47;

XX Best Local Similarity 78.9%; Pred. No. 4.1e+03;

XX Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

XX 1 GGTCTGCAGCGGATGCT 19

XX 11 | | | | | | | | | |

XX 18 GCGCTGCAGBGCATGTT 36

RESULT 12

AAH45300
ID AAH45300 standard; DNA: 27 BP.

XX AAH45300;

XX 10-SEP-2001 (first entry)

XX Human Bcl-2 mutagenic primer oligo-3 for 570A substitution.

XX Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; primer; ss.

XX Homo sapiens.

XX Synthetic.

XX WO200142459-A1.

XX 14-JUN-2001.

XX 07-DEC-2000; 2000WO-JP08667.

XX 09-DEC-1999; 99JP-0350427.

XX (HISM) HISAMITSU PHARM CO LTD.

XX Shibasaki F, Kuma H;

XX WPI: 2001-381681/40.

XX New apoptosis inhibitors, useful for treating apoptosis related

XX disorders -

XX Example 1: Page 10: 43pp: Japanese.

XX The invention relates to an apoptosis inhibitor comprising the

XX amino acid sequence of Bcl-2 protein in which at least one serine

XX residue is substituted by alanine or aspartic acid. The protein has

XX increased apoptosis inhibitory activity compared with the wild type

XX Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment

XX of disorders caused by apoptosis. The present sequence was used to

XX create a mutant Bcl-2 protein of the invention.

XX Sequence 27 BP; 2 A; 9 C; 12 G; 4 T; 0 other;

XX Query Match 69.5%; Score 13.2; DB 22; Length 27;

XX Best Local Similarity 83.3%; Pred. No. 5e+03;

XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

XX 2 GGTCTGCAGCGGATGCT 19

XX 11 | | | | | | | | | |

XX 1 GGTCTGCAGCGCGGCT 18

XX RESULT 13

XX ABK47064

XX ID ABK47064 standard; DNA: 27 BP.

XX ABK47064;

XX 05-JUN-2002 (first entry)

XX Adenovirus vector E3 region deletion PCR primer 4.

XX Adenovirus vector library; ss; primer: high throughput screening;

XX RCA; replication competent adenovirus; PCR.

XX Mastadenovirus Ad5.

XX US6340595-B1.

XX 22-JAN-2002.

XX 21-JUL-1999; 99US-0358036.


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XX 12-JUN-1998; 98US-0097239.
PR (GALA-) GALAPAGOS GENOMICS NV.
XX
XX Vogels R, Bout A, Van Es H, Schouten G;
PI WPI; 2002-224926/28.
XX
XX Library of expressible nucleic acids, useful for determining nucleic
PT acid function, comprises one or more adenoviral vectors capable of
XX transfecting a host cell with the nucleic acid
XX
XX Example 18: Column 63; 111pp; English.
XX
XX The invention relates to a library (I) of a multitude of unique
CC expressible nucleic acids (NA), comprises a number of compartments
CC (II), each consisting of one or more adenoviral vectors (III)
CC comprising at least one unique NA of (I) in an aqueous medium, where
CC (III) is capable of introducing the NA into a host cell (IV), is
CC capable of expressing the product of the NA in (IV), and is deleted in
CC a portion of the adenoviral genome necessary for replication. Also
CC included is a method for producing the library. The library is useful for
CC determining the function of at least one nucleic acid that is present.
CC The library uses high throughput generation of recombinant adenoviral
CC vector libraries containing one or more sample nucleic acids, followed by
CC high throughput screening of the adenoviral vector libraries in a host to
CC alter the phenotype of the host as a means of assigning a function to
CC expression product(s) of the sample nucleic acids. The entire process
CC lends itself to automation especially when implemented in a 96-well or
CC other multi-well format. The high throughput screening, using a number of
CC different in vitro assays, provides a means of efficiently obtaining
CC functional information in a relatively short period of time. The
CC member(s) of the recombinant adenoviral libraries that exhibit or induce
CC a desired phenotype in a host in vitro or in situ are identified to
CC reduce the libraries to a manageable number of recombinant adenoviral
CC vectors or clones which can be tested in vitro in an animal model.
CC Furthermore, the methods produce RCA-free adenoviral libraries. RCA
CC (replication competent adenovirus) contamination throughout the libraries
CC could become a major obstacle, especially if libraries are continuously
CC amplified for use in multiple screening programs. Additionally, a further
CC advantage is minimisation of the number of steps involved in the process.
CC There is no requirement for cloning each individual adenovirus before use
CC in a high throughput screening program. Other systems include one or more
CC steps in E. coli to achieve homologous recombination for the various
CC adenoviral plasmids necessary for vector generation. The present
CC sequence is a PCR primer used in the construction of the adenoviral
CC vector library of the invention.
XX
XX Sequence 27 BP; 3 A; 3 C; 13 G; 8 T; 0 other:
SO
Query Match 69.5%; Score 13.2; DB 24; Length 27;
Best Local Similarity 83.3%; Pred. No. 5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 2 GGTCTGACGCGCATGCT 19
| ||| ||||| |||
DB 8 GTTCTGAGCGGAGGCT 25
| ||| ||||| |||
RESULT 14
AA097259/c
ID AA097259 standard; cDNA; 33 BP.
XX
XX AA097259;
AC
XX
XX 28-DEC-1995 (first entry)
DT
XX
XX ATF-2 5' bridging primer.
DE
XX
XX Astrocyte-derived neurotrophic factor; ATF-1; neuron; GDNF;
KM primer; polymerase chain reaction; PCR; ss.
XX

```

```

OS Synthetic.
XX
XX Key Location/Qualifiers
XX misc_feature 1..17
FT
FT misc_feature /tag= a
FT /note= "bases 1-17 corresp. to GDNF bases 95-111"
FT /tag= b
FT /note= "bases 18-33 corresp. to GDNF bases 338-353"
XX
XX W09517203-A1.
XX
XX 29-JUN-1995.
XX
XX 22-DEC-1994; 94MO-US14771.
XX
XX 20-DEC-1994; 94US-0359480.
XX 22-DEC-1993; 93US-0172347.
XX 18-JUL-1994; 94US-0275709.
XX
XX (UYNE-) UNIV NEW JERSEY.
XX
XX Black IB, Dreyfuss CF, Schaar DG;
XX WPI: 1995-240472/31.
XX
XX New astrocyte-derived neurotrophic factor proteins - related nucleic
PT acid, vectors and transformed cells, useful for stimulating neuronal
XX cell survival and growth
XX
XX Example 1: Page 38; 107pp; English.
XX
XX The GDNF sequences deleted in human ATF-1 and ATF-2 cDNA clones
CC (AA097241-42, respectively) were analyzed by PCR using the bridging
CC primers given in AA097258-59. ATF mRNAs were expressed in substantia
CC nigra, caduate and putamen brain regions.
XX
XX Sequence 33 BP; 6 A; 16 C; 7 G; 4 T; 0 other:
SO
Query Match 69.5%; Score 13.2; DB 16; Length 33;
Best Local Similarity 83.3%; Pred. No. 5.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 GGGCTGACGCGCATGCG 18
| ||| ||||| |||
DB 28 GGGTTCGACGCGGAGG 11
| ||| ||||| |||
RESULT 15
AAT33615
ID AAT33615 standard; cDNA; 38 BP.
XX
XX AAT33615;
AC
XX
XX 30-NOV-1996 (first entry)
DT
XX
XX Murine VRF167 mRNA probe.
DE
XX
XX VRF: vascular endothelial growth factor; VEGF; SOM175; neuron;
KM astroglial proliferation; probe; ss.
XX
XX Synthetic.
XX
XX W09627007-A1.
XX
XX 06-SEP-1996.
XX
XX 22-FEB-1996; 96MO-AU00094.
XX
XX 22-DEC-1995; 95AU-0007274.
XX 02-MAR-1995; 95AU-0001457.
XX 20-NOV-1995; 95AD-0006647.
XX

```

PA (AMRA-) AMRAD OPERATIONS PTY LTD.

XX Grimmond S, Hayward NK, Larsson C, Nordenskjold M;
PI Weber G;

XX WP1: 1996-412774/41.

DR
XX New growth factor related to vascular endothelial growth factor -
PT useful for inducing astroglial proliferation and promoting neuronal
PT survival

XX Example 6, Page 27, 113pp; English.

CC Oligonucleotide probes (AAT33615 and AAT33616) are complementary to
CC nucleotides found in the mRNA coding for alternatively spliced
CC murine VRP167 (see also AAT33610). They, and other probes (see also
CC AAT33611 and AAT33614) for VRP186 (see also AAT33609), were used to
CC examine expression of murine VRP in pre- and post-natal mice. The 4
CC probes gave identical hybridisation patterns in all tissues examined.
CC VRP expression was detected in the E14 mouse embryo, esp. in the heart
CC and nervous system. In E17 embryos, and in young adult mice,
CC expression was confined to the heart and brown fat tissue.

XX SQ Sequence 38 BP; 6 A; 5 C; 18 G; 9 T; 0 other;

Query Match 69.5%; Score 13.2; DB 17; Length 38;
Best Local Similarity 83.3%; Pred. No. 5.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Caps 0;

OY 1 GCGCTCGACCGGATGC 18
||| ||| || |||||
DB 7 GCGCTGGAGTGGATGC 24

Search completed: November 28, 2002, 17:24:12
Job time : 177.575 secs

RENTI PAOLO (CA); RECH EXPERTISES ET DEV MEDICAU (CA)
FEATURES
source
1. .19
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="sense oligonucleotide for IL-3, IL-5 and GM-CSF"
BASE COUNT 4 a 10 c 3 g 2 t
ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCTGCACGGCGATGCT 19
|||||
Db 19 GGCTCTGCACGGCGATGCT 1

RESULT 2
LOCUS AX008656 19 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 9 from Patent WO9966037.
ACCESSION AX008656
VERSION AX008656.1 GI:9996180
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 19)
AUTHORS Renti, P.
TITLE Antisense oligonucleotides for treating or preventing atopic diseases and neoplastic cell proliferation
JOURNAL Patent: WO 9966037-A 9 23-DEC-1999;
RENTI PAOLO (CA); RECH EXPERTISES ET DEV MEDICAU (CA)
FEATURES
source
1. .19
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Antisense oligonucleotide inhibiting the common subunit of IL-3, IL-5 and GM-CSF human receptor"
BASE COUNT 2 a 3 c 10 g 4 t
ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCTGCACGGCGATGCT 19
|||||
Db 1 GGGCTGCACGGCGATGCT 19

RESULT 3
LOCUS AX008657 19 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 10 from Patent WO9966037.
ACCESSION AX008657
VERSION AX008657.1 GI:9996181
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 19)
AUTHORS Renti, P.
TITLE Antisense oligonucleotides for treating or preventing atopic diseases and neoplastic cell proliferation
JOURNAL Patent: WO 9966037-A 10 23-DEC-1999;
RENTI PAOLO (CA); RECH EXPERTISES ET DEV MEDICAU (CA)
FEATURES
source
1. .19
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Antisense oligonucleotide inhibiting the common

subunit of IL-3, IL-5 and GM-CSF human receptor"
BASE COUNT 2 a 3 c 9 g 5 t
ORIGIN

Query Match 94.7%; Score 18; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGTCTGCACGGCGATGCT 19
|||||
Db 1 GGTCTGCACGGCGATGCT 18

RESULT 4
LOCUS AX008658 19 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 11 from Patent WO9966037.
ACCESSION AX008658
VERSION AX008658.1 GI:9996182
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 19)
AUTHORS Renti, P.
TITLE Antisense oligonucleotides for treating or preventing atopic diseases and neoplastic cell proliferation
JOURNAL Patent: WO 9966037-A 11 23-DEC-1999;
RENTI PAOLO (CA); RECH EXPERTISES ET DEV MEDICAU (CA)
FEATURES
source
1. .19
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Antisense oligonucleotide inhibiting the common subunit of IL-3, IL-5 and GM-CSF human receptor"
BASE COUNT 3 a 3 c 10 g 3 t
ORIGIN

Query Match 94.7%; Score 18; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCTGCACGGCGATGCT 18
|||||
Db 2 GGGCTGCACGGCGATGCT 19

RESULT 5
LOCUS AX008662 19 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 15 from Patent WO9966037.
ACCESSION AX008662
VERSION AX008662.1 GI:9996186
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 19)
AUTHORS Renti, P.
TITLE Antisense oligonucleotides for treating or preventing atopic diseases and neoplastic cell proliferation
JOURNAL Patent: WO 9966037-A 15 23-DEC-1999;
RENTI PAOLO (CA); RECH EXPERTISES ET DEV MEDICAU (CA)
FEATURES
source
1. .19
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Antisense oligonucleotide inhibiting the common subunit of IL-3, IL-5 and GM-CSF human receptor"
BASE COUNT 2 a 3 c 8 g 6 t
ORIGIN

Query Match 89.5%; Score 17; DB 6; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GGTCTGACGGGATGCT 19
|||||
DB 1 GGTCTGACGGGATGCT 17

RESULT 6
LOCUS AX008659 19 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 12 from Patent WO9966037.
ACCESSION AX008659
VERSION AX008659.1 GI:9996183
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

Antisense oligonucleotides for treating or preventing atopic diseases and neoplastic cell proliferation
Patent: WO 9966037-A 12 23-DEC-1999,
RENZI P. (CA); RECH EXPERTISES ET DEV MEDICAU (CA)
JOURNAL
FEATURES
source
1. .19
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Antisense oligonucleotide inhibiting the common subunit of IL-3, IL-5 and GM-CSF human receptor"

BASE COUNT 3 a 4 c 9 g 3 t
ORIGIN

Query Match 84.2%; Score 16; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGTCTGACGGGAT 16
|||||
DB 4 GGGTCTGACGGGAT 19

RESULT 7
LOCUS ES0113 34 bp DNA linear PAT 31-JAN-2002
DEFINITION DNA fragment containing toluene monooxygenase gene, recombinant plasmid, transformed microorganism, process for decomposing halogenated aliphatic hydrocarbon and aromatic compound, and method for repairing environment by using the microorganism.
ACCESSION ES0113
VERSION ES0113.1 GI:18629391
KEYWORDS JP 2000224994-A/2.
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

DNA fragment containing toluene monooxygenase gene, recombinant plasmid, transformed microorganism, process for decomposing halogenated aliphatic hydrocarbon and aromatic compound, and method for repairing environment by using the microorganism
Patent: JP 2000224994-A 2 15-AUG-2000;
JOURNAL
COMMENT
OS Artificial Sequence
PN JP 2000224994-A/2
PD 15-AUG-2000
PR 03-DEC-1999 JP 1999345421
PI TETSUYA YANO, TAKESHI NOMOTO, TSUYOSHI IMAMURA
PC C12N15/09, A62D3/00, B01D53/70, B09C1/10, C02F3/34, C12N1/00, C12N1/21,
PC C12N9/04//C12N1/21, C12R1:19), (C12N9/04, C12R1:19), C12N15/00, B01D53/34,

PC B09B3/00
CC
FH Key location/Qualifiers
FT source 1. .34
FT /organism="Artificial Sequence",
location/Qualifiers

BASE COUNT 8 a 14 c 7 g 5 t
ORIGIN

Query Match 74.7%; Score 14.2; DB 6; Length 34;
Best Local Similarity 84.2%; Pred. No. 2.9e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGGTCTGACGGGATGCT 19
|||||
DB 31 GGGTCTGACGGGATGCT 13

RESULT 8
LOCUS A04394 43 bp DNA linear PAT 29-APR-1993
DEFINITION Oligonucleotide U5 for porcine growth hormone.
ACCESSION A04394
VERSION A04394.1 GI:344897
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

synthetic construct.
synthetic construct.
artificial sequences.
location/Qualifiers
source
1. .43
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 11 a 15 c 13 g 4 t
ORIGIN

Query Match 69.5%; Score 13.2; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 9e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GGTCTGACGGGATGCT 19
|||||
DB 18 GGTCTGACGGGATGCT 1

RESULT 9
LOCUS A04408 43 bp DNA linear PAT 29-APR-1993
DEFINITION Oligonucleotide L5 for porcine growth hormone.
ACCESSION A04408
VERSION A04408.1 GI:344911
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

synthetic construct.
synthetic construct.
artificial sequences.
location/Qualifiers
source
1. .43
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 10 a 10 c 15 g 8 t
ORIGIN

Query Match 69.5%; Score 13.2; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 9e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GGTCTGACGGGATGCT 19
|||||
DB 8 GGTCTGACGGGATGCT 25

TITLE Dna vaccines for pets and sport animals
JOURNAL Patent: WO 0077043-A 64 21-DEC-2000;
JOURNAL (FR) MERIAL

FEATURES
source Location/Qualifiers
1..33

/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"

BASE COUNT 6 a 11 c 10 g 6 t
ORIGIN

Query Match 66.3%; Score 12.6; DB 6; Length 33;
Best Local Similarity 78.9%; Pred. No. 1.8e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGCTCGCAGCGGATGGT 19
||| ||||| |||||
Db 31 GGTTCTGCAGCCACATGGT 13

RESULT 15
AX078782/c 33 bp DNA linear PAT 22-FEB-2001
LOCUS AX078782
DEFINITION Sequence 20 from Patent WO0105934.
ACCESSION AX078782
VERSION AX078782.1 GI:13158399

KEYWORDS
SOURCE

ORGANISM
synthetic construct.
synthetic construct.
artificial sequences.

REFERENCE 1 (bases 1 to 33)

AUTHORS Audonnet,J.C., Baudu,P.G. and Brunet,S.C.

TITLE Feline calicivirus genes and vaccines. In particular recombined

JOURNAL Patent: WO 0105934-A 20 25-JAN-2001;
MATERIAL (FR)

FEATURES
source Location/Qualifiers
1..33

/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"

BASE COUNT 6 a 11 c 10 g 6 t
ORIGIN

Query Match 66.3%; Score 12.6; DB 6; Length 33;
Best Local Similarity 78.9%; Pred. No. 1.8e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGCTCGCAGCGGATGGT 19
||| ||||| |||||
Db 31 GGTTCTGCAGCCACATGGT 13

Search completed: November 28, 2002, 18:20:38
Job time : 1105.97 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: November 28, 2002, 17:10:34 : Search time 1372.59 Seconds
(without alignments)
224.186 Million cell updates/sec

Title: US-09-719-737-18

Perfect score: 19

Sequence: 1 ctggcgcatcgatcgctctg 19

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estha:*
2: em_esthm:*
3: em_estln:*
4: em_estln:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_jny:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_alter:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	12.4	65.3	38	17	A2834919
C 2	12.2	64.2	29	17	TA59B050
C 3	12	63.2	31	12	BF181705
C 4	12	63.2	38	17	BH792093
C 5	12	63.2	49	17	AZ472469
C 6	11.8	62.1	35	13	BJ084423

Result No.	Score	Query Match	Length	DB ID	Description
C 7	11.8	62.1	36	17	AL762128
C 8	11.8	62.1	37	17	A2384612
C 9	11.8	62.1	44	17	BH000259
C 10	11.8	62.1	45	17	A2309922
C 11	11.8	62.1	48	17	BH791856
C 12	11.6	61.1	33	17	A2391565
C 13	11.6	61.1	35	12	BF793800
C 14	11.6	61.1	40	17	A2807388
C 15	11.6	61.1	41	17	A2774224
C 16	11.4	60.0	39	17	A2892211
C 17	11.4	60.0	41	17	A2437628
C 18	11.4	60.0	44	10	AV843723
C 19	11.4	60.0	48	17	A2602280
C 20	11.2	58.9	31	9	AA181661
C 21	11.2	58.9	31	13	B1154945
C 22	11.2	58.9	33	13	B1103577
C 23	11.2	58.9	34	9	AA109657
C 24	11.2	58.9	49	9	AA691710
C 25	11	57.9	25	17	A2648037
C 26	11	57.9	30	17	A2949156
C 27	11	57.9	32	10	AV834034
C 28	11	57.9	32	10	AV956830
C 29	11	57.9	32	17	A2441593
C 30	11	57.9	32	17	A2600248
C 31	11	57.9	32	17	A2816444
C 32	11	57.9	35	17	A2482003
C 33	11	57.9	35	17	A2581423
C 34	11	57.9	35	17	A2860292
C 35	11	57.9	35	17	BH128269
C 36	11	57.9	43	9	A1496922
C 37	11	57.9	43	17	A2834960
C 38	11	57.9	44	13	BJ033250
C 39	11	57.9	44	17	A2662473
C 40	11	57.9	45	17	A2839967
C 41	11	57.9	46	9	AA652871
C 42	11	57.9	47	17	A2481505
C 43	11	57.9	49	9	A1744224
C 44	11	57.9	50	9	AU102583
C 45	11	57.9	50	9	AU105201

ALIGNMENTS

RESULT 1
A2834919/c
LOCUS
DEFINITION
2M0117D21R Mouse 10kb Plasmid UGCM library Mus musculus genomic
clone UUGC2M0117D21 R. DNA sequence.
A2834919
ACCESSION
A2834919.1 GI:3004827
VERSION
A2834919.1
KEYWORDS
GSS
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 (bases 1 to 38)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,
'M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid Inserts
Unpublished (2000)
Contact: Robert B. Weiss,
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

JOURNAL COMMENT

Plate: 0117 row: D column: 21
Seq primer: CACACAGCAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 38.
Location/Qualifiers

FEATURES

SOURCE

1. 38
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U00C2M0117D21"
/clone_lib="Mouse 10kb plasmid U00C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42ny: Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1147321419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 15 a 10 c 7 g 6 t
ORIGIN

Query Match 65.3% Score 12.4; DB 17; Length 38;
Best Local Similarity 92.9%; Pred. No. 4e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CTGGCCATCATGCTC 15
||||| ||||| |||||
Db 30 TGGCTCATCATGCTC 17

RESULT 2
LOCUS TA598050 29 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 59b05, reverse sequence.
ACCESSION AL456550
VERSION AL456550.1 GI:11858271
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 29)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).
Email: nh@sanger.ac.uk
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.
Location/Qualifiers

FEATURES

SOURCE

1. 29
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="59b05"
/clone_lib="59b05"

BASE COUNT 5 a 11 c 6 g 7 t
ORIGIN

Query Match 64.2% Score 12.2; DB 17; Length 29;
Best Local Similarity 82.4%; Pred. No. 4.3e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CTGGCCATCATGCTC 17
||||| ||||| |||||
Db 13 CTGGCCCTCAGGCTC 29

RESULT 3
LOCUS BF181705 31 bp mRNA linear EST 31-OCT-2000
DEFINITION 60180518F1 NCI-CGAP_Mam5 Mus musculus cDNA clone IMAGE:4036180 5',
mRNA sequence.
ACCESSION BF181705
VERSION BF181705.1 GI:11059847
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 31)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgabs-r@mail.nih.gov
Tissue Procurement: Iohar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1AM0311 row: d column: 05
High quality sequence stop: 31.
Location/Qualifiers

FEATURES

SOURCE

1. 31
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:4036180"
/clone_lib="NCI-CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: PCMV-SF0RT6; Site: 1; Salt:
Site: 2; NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Iohar Hennighausen/Robin Humphreys,
NIH"

BASE COUNT 5 a 10 c 10 g 6 t
ORIGIN

Query Match 63.2% Score 12; DB 12; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGCCATCATG 12
||||| ||||| |||||

Db 3 CTGGGCCATCAG 14

RESULT 4
LOCUS BH792093/C

DEFINITION BH792093 38 bp DNA linear GSS 02-Apr-2002
SALK_062674.45.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_062674.45.30.x, DNA
sequence.

ACCESSION BH792093
VERSION BH792093.1 GI:19888485
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi-
s (bases 1 to 38)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,
C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At5g05390.
Class: TDNA tagged.
Location/Qualifiers
1. 38
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_062674.45.30.x"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/cdna_protocols.html"

BASE COUNT 12 a 7 c 13 g 6 t

ORIGIN

Query Match 63.2%; Score 12; DB 17; Length 38;
Best Local Similarity 100.0%; Pred. No. 6.2e+04;
Matches 12: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGGCCATCAG 12
|||||
Db 34 CTGGGCCATCAG 23

RESULT 5
LOCUS AZ472469

DEFINITION AZ472469 49 bp DNA linear GSS 04-OCT-2000
clone UUGC1M0287P09 R, DNA sequence.

ACCESSION AZ472469
VERSION AZ472469.1 GI:10630594
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

JOURNAL COMMENT
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0287 row: P column: 09
Seq primer: CACACGACAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 49.
Location/Qualifiers
1. 49
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0287P09"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, F1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>) The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114[g14732114]p129072.1), a copy-number
inducible derivative of plasmid p1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 10 a 11 c 15 g 13 t

ORIGIN

Query Match 63.2%; Score 12; DB 17; Length 49;
Best Local Similarity 100.0%; Pred. No. 7.1e+04;
Matches 12: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GGCCATCAGTG 14
|||||
Db 29 GGCCATCAGTG 40

RESULT 6
LOCUS BJ084423/C

DEFINITION BJ084423 35 bp mRNA linear EST 12-DEC-2001
laevis cDNA clone X1089c18.3', mRNA sequence.

ACCESSION BJ084423
VERSION BJ084423.1 GI:17579964
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 35)

AUTHORS	Kiyama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T., and Kohara, Y.									
TITLE	Expressed genes in <i>X. laevis</i> embryo									
JOURNAL	Unpublished (2001)									
COMMENT	Contact: Tadasu Shin-i Center for Genetic Resource Information National Institute of Genetics 111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tsuhigenes.nig.ac.jp									
FEATURES	location/Qualifiers									
Source	1..35									
	/organism="Xenopus laevis"									
	/db_xref="taxon:8355"									
	/clone="XL089c18"									
	/clone_lib="NIBB Mochii normalized Xenopus tailbud library"									
	/tissue_type="whole embryo"									
	/dev_stage="stage 25"									
	/note="vector: pBSR3; Site_1: NotI; Site_2: EcoRI; CDNAS were oligo-dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute)."									
BASE COUNT	9 a 6 c 9 g 10 t 1 others									
ORIGIN										
Query Match	62.1%; Score 11.8; DR 13; length 35;									
Best Local Similarity	86.7%; Pred. No. 7.3e+04;									
Matches 13; Conservative	0; Mismatches 2; Indels 0; Gaps 0;									
QY	4 GCCCATCAGTCTCT 18									
	111111111111									
DB	29 GCCAATCAGACTCT 15									
RESULT 7										
AL762128/c										
LOCUS	36 bp DNA linear GSS 18-JUN-2002									
DEFINITION	Arabidopsis thaliana T-DNA flanking sequence GK-021B05-013592, genomic survey sequence.									
ACCESSION	AL762128									
VERSION	AL762128.1 GI:21506683									
KEYWORDS	GSS.									
SOURCE	thale cress.									
ORGANISM	Arabidopsis thaliana									
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots; Rosidae; eustosids II; Brassicales; Brassicaceae; Arabidopsis.									
REFERENCE	1 Strizhov, N., Li, Y., Rosso, M., Vliehoveer, P., Dekker, K., Seadler, H. and Weisshaar, B.									
AUTHORS	A pipeline for automated high-throughput generation of FSNs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines									
TITLE	Unpublished									
JOURNAL	2									
REFERENCE	Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B.									
AUTHORS	A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics									
JOURNAL	Unpublished									
REFERENCE	3 (bases 1 to 36)									
AUTHORS	Rosso, M., Li, Y., Strizhov, N. and Weisshaar, B.									
TITLE	Direct Submission									
JOURNAL	Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforshung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany									
COMMENT	This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone t5e7. The sequences are generated at the MPI for plant breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German plant genomics program designated 'GABI'. Information on line availability can be found at:									

http://www.mpiz-koeln.mpg.de/GABI-Kat/.

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location/Qualifiers
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/oranism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-021B05-013692"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC106. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thaliana nuclear genome sequence were
processed for submission. T-DNA derived sequences were
removed"

BASE COUNT      7 a      13 c      7 g      9 t

Query Match      62.1%   Score 11.8; DB 17;   Length 36;
Best Local Similarity 86.7%:   Pred. No. 7,5e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 TGGGCCATCAGTCT 16
      1111 11111111
Db      31 TGGGGATCAGTCT 17

RESULT 8
LOCUS      AZ384612      37 bp      DNA      linear      GSS 02-OCT-2000
DEFINITION 1M0142008R Mouse 10kb plasmid UUGC1M 1library Mus musculus genomic
ACCESSION  AZ384612
VERSION     AZ384612
KEYWORDS    GSS.
SOURCE      house mouse.
ORANISM     Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 37)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0142 row: 0 column: 08
            Seq primer: CACACGAGCAACACGCTAAGACC
            Class: plasmid ends
            High quality sequence stop: 37.
location/Qualifiers
1..37
/oranism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0142008"
/clone_lib="Mouse 10kb plasmid UUGC1M 1library"
/sex="Male"
/lab_host="D. Coll strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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BASE COUNT      5 a      8 c      7 g      13 t
ORIGIN
Query Match      61.1%; Score 11.6; DB 17; Length 33;
Best Local Similarity 77.8%; Pred. No. 8.8e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY      2  TGGGCCATCAGTCTCTG 19
        ||||| 11111 11111
Db      12  TGGGACATCATCTCTTTG 29

RESULT 13
LOCUS      BF793800
DEFINITION 602254477F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4346510 5',
            mRNA sequence.
ACCESSION  BF793800
VERSION     BF793800.1 GI:12098863
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 35)
            NIH-MGC http://mgs.mci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            JOURNAL  Unpublished (1999)
            COMMENT  Contact: Robert Strausberg, Ph.D.
                     Email: cga@bbs-remail.nih.gov
                     Tissue Procurement: ATCC
                     CDNA Library Preparation: Life Technologies, Inc.
                     CDNA Library Arranged by: The I.M.A.G.E. Consortium (LLNL)
                     DNA Sequencing by: Incyte Genomics, Inc.
                     Clone distribution: MGC clone distribution information can be
                     found through the I.M.A.G.E. Consortium/LLNL at:
                     http://image.llnl.gov
                     Plate: L14M9968 row: j column: 19
                     High quality sequence stop: 35.
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        1..35
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            /db_xref="taxon:9606"
            /clone_image="4346510"
            /clone_lib="NIH_MGC_84"
            /tissue_type="adrenal cortex carcinoma, cell line"
            /lab_host="DH10B (phage-resistant)"
            /note="Organ: adrenal gland. Vector: pCMV-SPOK6; Site_1:
            NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT
            primed. Average insert size 1.229 kb. Library enriched for
            full-length clones and constructed by Life Technologies.
            Note: this is a NIH-MGC library."
BASE COUNT      3 a      15 c      8 g      9 t
ORIGIN
Query Match      61.1%; Score 11.6; DB 12; Length 35;
Best Local Similarity 77.8%; Pred. No. 9.1e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY      1  CTGGCCATCAGTCTCT 18
        ||||| 11111 11111
Db      16  CTGGGCCACCATAGCCCT 33

RESULT 14
LOCUS      A2807388
DEFINITION 2M0070010F Mouse 10kb plasmid UUCGCM library Mus musculus genomic
            clone UUCG2M0070010 F, DNA sequence.
ACCESSION  A2807388
VERSION     A2807388.1 GI:12971685
KEYWORDS   GSS.
SOURCE     house mouse.

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ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 40)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
            and Wright,D., Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
            84112, USA
            Tel.: 801 585 5606
            Fax: 801 585 7177
            Email: dunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0070 row: 0 column: 10
            Seq primer: CGTTGTAACGACGCCACG
            Class: plasmid ends
            High quality sequence stop: 40.
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            /organism="Mus musculus"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone_image="UUCG2M0070010"
            /clone_lib="Mouse 10kb plasmid UUCGCM library"
            /sex="Male"
            /lab_host="E. Coli strain XL10-gold, p1-resistant, F-"
            /note="Vector: pMD42ny: Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pMD42 (9114732114[9b]AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-gold (Stratagene) cells
            and selected for ampicillin resistance."
BASE COUNT      6 a      6 c      17 g      11 t
ORIGIN
Query Match      61.1%; Score 11.6; DB 17; Length 40;
Best Local Similarity 77.8%; Pred. No. 9.8e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY      1  CTGGCCATCAGTCTCT 18
        ||||| 11111 11111
Db      13  CTGGGCCATCATCTTTT 30

RESULT 15
LOCUS      A2774224
DEFINITION 2M0003E19F Mouse 10kb plasmid UUCGCM library Mus musculus genomic
            clone UUCG2M0003E19 F, DNA sequence.
ACCESSION  A2774224
VERSION     A2774224.1 GI:12899427
KEYWORDS   GSS.
SOURCE     house mouse.

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ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 41)

REFERENCE
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly
 , M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112 USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0003 row: E column: 19
 Seq primer: CGTTGTAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 41.

FEATURES
 Location/Qualifiers
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 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG2M0003E19"
 /clone_1lb="Mouse 10kb plasmid UUCG1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD42uv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g1147321149b1AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."
 15 t

BASE COUNT
 6 a 9 c 11 g 15 t

ORIGIN
 Query Match 61.1%; Score 11.6; DB 17; Length 41;
 Best Local Similarity 77.8%; Pred. No. 9.9e+04;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 0Y 1 CTGGGCATCACTGCTCT 18
 11 | | | | | | | | | |
 DB 16 CTTCACATCACTGCTCT 33

Search completed: November 28, 2002, 19:30:47
 Job time : 1375.59 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 28, 2002, 17:15:39 : Search time 39.9655 Seconds
(without alignments)
183,088 Million cell updates/sec

Title: US-09-719-737-18

Perfect score: 19

Sequence: 1 cggagcgcacgctcctg 19

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 341543 seqs, 192557720 residues

Total number of hits satisfying chosen parameters: 177872

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications, NA:*

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- 2: /cgn2.6/ptodata/1/pubpna/PCCT_NEW_PUB.seq:*
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- 12: /cgn2.6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2.6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2.6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	13	68.4	36	10	US-09-504-231A-1780
C 2	13	68.4	36	10	US-09-274-553D-1780
C 3	12.8	67.4	17	10	US-09-866-108-6582
C 4	12.8	67.4	17	10	US-09-866-108-6582
C 5	12.8	67.4	25	10	US-09-866-108-6583
C 6	12.8	67.4	25	10	US-09-792-232-4
C 7	12.8	67.4	25	10	US-09-866-108-11474
C 8	12.8	67.4	25	10	US-09-866-108-11475
C 9	12.8	67.4	25	10	US-09-866-108-11476
C 10	12.8	67.4	25	10	US-09-866-108-11477
C 11	12.8	67.4	25	10	US-09-866-108-11478
C 12	12.8	67.4	25	10	US-09-866-108-11479
C 13	12.8	67.4	25	10	US-09-866-108-11480
C 14	12.8	67.4	25	10	US-09-866-108-11481
C 15	12.8	67.4	25	10	US-09-866-108-11482
C 16	12.6	66.3	43	10	US-09-866-108-11483
C 17	12.6	66.3	43	10	US-09-766-378A-2
C 18	12.4	65.3	44	10	US-09-848-164-40
C 19	12.4	65.3	17	9	US-09-872-462-249
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20	12.4	65.3	17	9	US-09-872-462-251	Sequence 251, App
21	12.4	65.3	17	9	US-09-872-462-252	Sequence 252, App
C 22	12.4	65.3	20	10	US-09-820-339A-22	Sequence 22, App1
23	12.4	65.3	25	9	US-09-872-462-460	Sequence 460, App
24	12.4	65.3	25	9	US-09-872-462-461	Sequence 461, App
25	12.4	65.3	25	9	US-09-872-462-462	Sequence 462, App
26	12.4	65.3	25	9	US-09-872-462-463	Sequence 463, App
27	12.4	65.3	25	9	US-09-872-462-464	Sequence 464, App
28	12.4	65.3	25	9	US-09-872-462-465	Sequence 465, App
29	12.4	65.3	25	9	US-09-872-462-466	Sequence 466, App
30	12.4	65.3	25	9	US-09-872-462-467	Sequence 467, App
C 31	12.4	65.3	30	10	US-09-898-541-24	Sequence 24, App1
C 32	12.2	64.2	20	10	US-09-854-883-193	Sequence 193, App
C 33	12.2	64.2	31	10	US-09-801-274-1400	Sequence 1400, App
34	12	63.2	17	9	US-09-872-462-253	Sequence 253, App
35	12	63.2	17	9	US-09-872-462-254	Sequence 254, App
36	12	63.2	31	10	US-09-801-274-1721	Sequence 1721, App
37	12	63.2	39	10	US-09-894-633A-7	Sequence 7, App1
C 38	11.8	62.1	17	10	US-09-866-108-6581	Sequence 6581, App
C 39	11.8	62.1	17	10	US-09-866-108-6584	Sequence 6584, App
40	11.8	62.1	18	9	US-09-905-291A-387	Sequence 387, App
41	11.8	62.1	18	9	US-09-909-320-387	Sequence 387, App
42	11.8	62.1	18	10	US-09-909-088B-387	Sequence 387, App
C 43	11.8	62.1	25	10	US-09-866-108-11473	Sequence 11473, App
C 44	11.8	62.1	25	10	US-09-866-108-11484	Sequence 11484, App
C 45	11.6	61.1	30	9	US-09-898-234-9	Sequence 9, App1

ALIGNMENTS

RESULT 1
US-09-504-231A-1780/c
: Sequence 1780, Application US/09504231A
: Patent No. US20020013458A1
GENERAL INFORMATION:
: APPLICANT: Blatt, Lawrence
: APPLICANT: McSwigen, James
: APPLICANT: Roberts, Beth
: APPLICANT: Pavco, Pamela
: APPLICANT: Macejak, Dennis
: TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS REL
: FILE REFERENCE: rpl 247/282
: CURRENT APPLICATION NUMBER: US/09/504, 231A
: CURRENT FILING DATE: 2000-02-15
: PRIOR APPLICATION NUMBER: 09/274, 553
: PRIOR FILING DATE: 1999-03-23
: PRIOR APPLICATION NUMBER: 09/257, 608
: PRIOR FILING DATE: 1999-02-24
: PRIOR APPLICATION NUMBER: 60/100, 842
: PRIOR FILING DATE: 1998-09-18
: PRIOR APPLICATION NUMBER: 60/083, 217
: NUMBER OF SEQ ID NOS: 3242
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 1780
: LENGTH: 36
: TYPE: RNA
: FEATURE: Artificial Sequence
: OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Mo

Query Match 68.4% Score 13: DB 10: Length 36:
Best Local Similarity 100.0% Pred. No. 7.1e+02:
Matches 13: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 7 CATCAGTCCTCTG 19
DB 13 CATCAGTCCTCTG 1

RESULT 2
US-09-274-553D-1780/C
Sequence 1780, Application US/09274553D
Patent No. US2002008225A1
GENERAL INFORMATION:
APPLICANT: Blatt, Lawrence
APPLICANT: McSwiggen, James
APPLICANT: Roberts, Beth
APPLICANT: Pavco, Pamela
APPLICANT: Macejak, Dennis
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
FILE REFERENCE: FPI 247/282
CURRENT APPLICATION NUMBER: US/09/274,553D
CURRENT FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 09/257,608
PRIOR FILING DATE: 1999-02-24
PRIOR APPLICATION NUMBER: 60/100,842
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/083,217
PRIOR FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 3148
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1780
LENGTH: 36
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-09-274-553D-1780

Query Match 68.4%; Score 13; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CATGAGTCCTCTG 19
|||||
DB 13 CATGAGTCCTCTG 1

RESULT 3
US-09-866-108-6582/C
Sequence 6582, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AROMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aromica Sequence Listing Engine
SEQ ID NO 6582
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-6582

Query Match 67.4%; Score 12.8; DB 10; Length 17;
Best Local Similarity 87.5%; Pred. No. 8.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGGCCATCATGCT 16
|||||
DB 17 CTGGCCCTCATGCT 2

RESULT 4
US-09-866-108-6583/C
Sequence 6583, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:

APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AROMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687

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; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO: 6583
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-6583

Query Match
Best Local Similarity 67.4%; Score 12.8; DB 10; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGGGCGCATCAGTCT 16
    ||||| |||||
Db 16 CTGGGCGCATCAGTCT 1

RESULT 5
US-09-795-232-4/c
; Sequence 4, Application US/09795232
; Patent No. US20010012627A1
; GENERAL INFORMATION:
; APPLICANT: Anthony M. Brown
; APPLICANT: Conrad Gerald Chapman
; APPLICANT: Israel Simon Gloger
; APPLICANT: Joanne Rachel Evans
; APPLICANT: William Cairns
; APPLICANT: Hugh Jonathan Herdon
; FILE REFERENCE: GP-30176-D1
; CURRENT APPLICATION NUMBER: US/09/795,232
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/182,728
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 9818890.7
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-795-232-4

Query Match
Best Local Similarity 67.4%; Score 12.8; DB 10; Length 25;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGGGCGCATCAGTCT 16
    ||||| |||||
Db 21 CTGGGCGCATCAGTCT 6

RESULT 6
US-09-866-108-11474/c
; Sequence 11474, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
```

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; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO: 11474
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-11474

Query Match
Best Local Similarity 67.4%; Score 12.8; DB 10; Length 25;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGGGCGCATCAGTCT 16
    ||||| |||||
Db 25 CTGGGCGCATCAGTCT 10

RESULT 7
US-09-866-108-11475/c
; Sequence 11475, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
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;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 60/266,860
;; PRIOR FILING DATE: 2001-02-05
;; NUMBER OF SEQ ID NOS: 15752
;; SOFTWARE: Acomica Sequence Listing Engine
;; SEQ ID NO 11475
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-866-108-11475
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```
Query Match 67.4%; Score 12.8; DB 10; Length 25;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy 1 CTGGCCATCAGTGCT 16
    ||||| |||||
Db 24 CTGGACCCCTCAGTGCT 9
```

RESULT 8
US-09-866-108-11476/c

Sequence 11476, Application US/09866108
Patent No. US20020048800A1

GENERAL INFORMATION:

APPLICANT: GU, Yizhong

APPLICANT: JI, Yonggang

APPLICANT: PENN, Sharon G.

APPLICANT: HANZEL, David K.

APPLICANT: RANK, David R.

APPLICANT: CHEN, Wensheng

APPLICANT: SHANNON, Mark

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: A60MICA-7

CURRENT APPLICATION NUMBER: US/09/866,108

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: GB 24263,6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

```
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 60/266,860
;; PRIOR FILING DATE: 2001-02-05
;; NUMBER OF SEQ ID NOS: 15752
;; SOFTWARE: Acomica Sequence Listing Engine
;; SEQ ID NO 11476
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-866-108-11476
```

```
Query Match 67.4%; Score 12.8; DB 10; Length 25;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
Oy 1 CTGGCCATCAGTGCT 16
    ||||| |||||
Db 23 CTGGACCCCTCAGTGCT 8
```

RESULT 9

US-09-866-108-11477/c

Sequence 11477, Application US/09866108

Patent No. US20020048800A1

GENERAL INFORMATION:

APPLICANT: GU, Yizhong

APPLICANT: JI, Yonggang

APPLICANT: PENN, Sharon G.

APPLICANT: HANZEL, David K.

APPLICANT: RANK, David R.

APPLICANT: CHEN, Wensheng

APPLICANT: SHANNON, Mark

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: A60MICA-7

CURRENT APPLICATION NUMBER: US/09/866,108

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: GB 24263,6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 60/266,860

PRIOR FILING DATE: 2001-02-05

NUMBER OF SEQ ID NOS: 15752

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SOFTWARE: Aecomica Sequence Listing Engine
SEQ ID NO 11477
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-11477
```

```
Query Match      67.4%; Score 12.8; DB 10; Length 25;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 CTGGGCCATCAGTCT 16
        ||||| || ||||| |||
DB      22 CTGGACCTCAGTCT 7
```

```
RESULT 10
US-09-866-108-11478/c
Sequence 11478, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AECOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aecomica Sequence Listing Engine
SEQ ID NO 11478
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-11478
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```
Query Match      67.4%; Score 12.8; DB 10; Length 25;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 CTGGGCCATCAGTCT 16
        ||||| || ||||| |||
DB      21 CTGGACCTCAGTCT 6
```

```
RESULT 11
US-09-866-108-11479/c
Sequence 11479, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AECOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263,5
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aecomica Sequence Listing Engine
SEQ ID NO 11479
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-11479
```

```
Query Match      67.4%; Score 12.8; DB 10; Length 25;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 CTGGGCCATCAGTCT 16
        ||||| || ||||| |||
DB      20 CTGGACCTCAGTCT 5
```

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RESULT 12
US-09-866-108-11480/c
Sequence 11480, Application US/09866108
Patent No. US20020048800A1
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```

; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 11480
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-11480

Query Match      67.4% Score 12.8; DB 10; Length 25;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1 CTGGCCCATCAGTCT 16
        ||| || |||||
DB      19 CTGACCCCTCAGTCT 4

RESULT 13
US-09-866-108-11481/c
; Sequence 11481, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
```

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; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR FILING DATE: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 11481
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-11481

Query Match      67.4% Score 12.8; DB 10; Length 25;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1 CTGGCCCATCAGTCT 16
        ||| || |||||
DB      18 CTGACCCCTCAGTCT 3

RESULT 14
US-09-866-108-11482/c
; Sequence 11482, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 11482
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-11482
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Query Match      67.4%  Score 12.8;  DB 10;  Length 25;
Best Local Similarity 87.5%;  Pred. No. 8.5e+02;
Matches 14;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY 1 CTGGGCGCATCACTGCT 16
    |||| || |||||
Db 17 CTGGACCTCACTGCT 2
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RESULT 15
US-09-866-108-11483/C
; Sequence 11483, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR FILING DATE: 2001-05-25.
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 11483
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-11483
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Query Match      67.4%  Score 12.8;  DB 10;  Length 25;
Best Local Similarity 87.5%;  Pred. No. 8.5e+02;
Matches 14;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY 1 CTGGGCGCATCACTGCT 16
    |||| || |||||
Db 16 CTGGACCTCACTGCT 1
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Search completed: November 28, 2002, 19:35:04
Job time : 39.9655 secs
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 28, 2002, 17:12:29 ; Search time 38.3276 Seconds

(without alignments)
152.028 Million cell updates/sec

Title: US-09-719-737-18

Perfect score: 19

Sequence: 1 ctggcgcatcagtgctctg 19

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/prodata/2/ina/5A.COMB.seq: *
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4: /cgn2_6/prodata/2/ina/6B.COMB.seq: *
5: /cgn2_6/prodata/2/ina/PCRTUS.COMB.seq: *
6: /cgn2_6/prodata/2/ina/Dackfilles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	15.8	83.2	45	2	US-08-687-355A-14
2	15.8	83.2	45	4	US-09-407-367-14
3	14.8	77.9	45	2	US-08-687-355A-13
4	14.8	77.9	45	4	US-09-407-367-13
5	14.4	75.8	20	1	US-08-742-023-15
6	14.4	75.8	20	3	US-08-968-505-15
7	13.2	69.5	33	3	US-09-233-506-11
8	13.2	69.5	27	4	US-08-584-040-4815
9	12.8	67.4	25	4	US-09-182-728A-4
10	12.8	67.4	25	4	US-09-795-232-4
11	12.6	66.3	43	4	US-08-596-190A-2
12	12.6	66.3	44	2	US-08-596-387B-40
13	12.6	66.3	44	4	US-09-067-615-40
14	12.6	66.3	44	5	PCR-US95-09816A-40
15	12.4	65.3	18	3	US-08-773-731A-12
16	12.4	65.3	30	4	US-09-230-199-24
17	12.4	65.3	31	1	US-08-390-850-222
18	12.4	65.3	31	1	US-08-390-850-222
19	12.4	65.3	31	1	US-08-390-850-224
20	12.4	65.3	31	1	US-08-435-634-222
21	12.4	65.3	31	1	US-08-435-634-223
22	12.4	65.3	31	1	US-08-435-634-224
23	12.4	65.3	31	2	US-08-859-998-167
24	12.4	65.3	31	4	US-09-225-928-167
25	12.4	65.3	40	4	US-09-485-737B-35
26	12.2	64.2	20	4	US-09-487-368A-193
27	12.2	64.2	36	4	US-09-101-126-13

C	28	12.2	64.2	45	2	US-08-944-982-1	Sequence 1, Appl1
C	29	12	63.2	20	4	US-09-429-322-61	Sequence 61, Appl1
C	30	12	63.2	21	3	US-09-009-913-19	Sequence 19, Appl1
C	31	12	63.2	27	4	US-08-584-040-1443	Sequence 1443, Ap
C	32	12	63.2	27	4	US-08-584-040-3326	Sequence 3326, Ap
C	33	12	63.2	27	4	US-08-584-040-5379	Sequence 5379, Ap
C	34	12	63.2	36	1	US-08-291-932A-568	Sequence 568, App
C	35	11.8	62.1	20	2	US-08-117-952-476	Sequence 476, App
C	36	11.8	62.1	27	3	US-08-513-974B-121	Sequence 121, App
C	37	11.8	62.1	36	1	US-08-484-686B-18	Sequence 18, Appl1
C	38	11.8	62.1	36	4	US-08-463-180B-18	Sequence 18, Appl1
C	39	11.8	62.1	45	1	US-08-171-389-257	Sequence 257, App
C	40	11.8	62.1	45	1	US-08-167-939A-13	Sequence 13, Appl1
C	41	11.8	62.1	45	1	US-08-123-936-257	Sequence 257, App
C	42	11.8	62.1	45	1	US-08-567-538-13	Sequence 13, Appl1
C	43	11.8	62.1	45	2	US-08-475-228A-257	Sequence 257, App
C	44	11.8	62.1	45	3	US-08-482-080A-257	Sequence 257, App
C	45	11.8	62.1	45	4	US-09-354-947-257	Sequence 257, App

ALIGNMENTS

RESULT 1
US-08-687-355A-14/C
Sequence 14, Application US/08687355A
Patent No. 5989834
GENERAL INFORMATION:
APPLICANT: Synaptic Pharmaceutical Corporation
TITLE OF INVENTION: NUCLEIC ACID ENCODING NEUROPEPTIDE
TITLE OF INVENTION: Y/PEPTIDE YX (Y2) RECEPTORS AND USES THEREOF
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,355A
FILING DATE: NO. 5989834ember 26, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44742-A-PC/JP/MAT
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-687-355A-14

Query Match 83.2%; Score 15.8; DB 2; Length 45;
Best Local Similarity 89.5%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CY 1 CTGGCGCATCAGTCTCTG 19
DB 43 CTGGCGCATCAGTCTCTG 25

RESULT 2
US-09-407-367-14/C
Sequence 14, Application US/09407367
Patent No. 6420532
GENERAL INFORMATION:
APPLICANT: Christophe P.G. Gerald, et al.
TITLE OF INVENTION: METHOD OF OBTAINING COMPOSITIONS COMPRISING Y2 SPECIFIC COMPO
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/407,367
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44742-AA-PCT-US/JPM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-407-367-14
Query Match 83.2%; Score 15.8; DB 4; Length 45;
Best Local Similarity 89.5%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CY 1 CTGGCCATCATGCTCTG 19
|||||
DB 43 CTGGGCATCATGCTCCCTG 25
RESULT 3
US-08-687-355A-13
Sequence 13, Application US/08687355A
Patent No. 5989834
GENERAL INFORMATION:
APPLICANT: Synaptic Pharmaceutical Corporation
TITLE OF INVENTION: NUCLEIC ACID ENCODING NEUROPEPTIDE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,355A
FILING DATE: NO. 5989834ember 26, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44742-A-PCT-US/JPM/MAT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-687-355A-13
Query Match 77.9%; Score 14.8; DB 2; Length 45;
Best Local Similarity 88.9%; Pred. No. 53;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CY 1 CTGGCCATCATGCTCT 18
|||||
DB 28 CTGGGCATCATGCTCCCT 45
RESULT 4
US-09-407-367-13
Sequence 13, Application US/09407367
Patent No. 6420532
GENERAL INFORMATION:
APPLICANT: Christophe P.G. Gerald, et al.
TITLE OF INVENTION: METHOD OF OBTAINING COMPOSITIONS COMPRISING Y2 SPECIFIC COM
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/407,367
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44742-AA-PCT-US/JPM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-407-367-13

Query Match 77.9%; Score 14.8; DB 4; Length 45;
Best Local Similarity 88.9%; Pred. No. 53;
Matches 16: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGGGCATCAGTCTCTG 18
DB 28 CTGGGCATCAGTCTCTG 45

RESULT 5

US-08-742-023-15
Sequence 15, Application US/08742023
Patent No. 5800997

GENERAL INFORMATION:

APPLICANT: Beck, James J.
TITLE OF INVENTION: Detection of Maize Fungal Pathogens
TITLE OF INVENTION: Using the Polymerase Chain Reaction
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,023
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer JBS86"

US-08-742-023-15

Query Match 75.8%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 76;
Matches 15: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 GGCCATCAGTCTCTG 19
DB 2 GGCCATCAGTCTCTG 17

RESULT 6

US-08-968-505-15
Sequence 15, Application US/08968505
Patent No. 6071698

GENERAL INFORMATION:

APPLICANT: Beck, James J.
TITLE OF INVENTION: Detection of Maize Fungal Pathogens
TITLE OF INVENTION: Using the Polymerase Chain Reaction
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown

STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,505
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/742,023
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer JBS86"

US-08-968-505-15

Query Match 75.8%; Score 14.4; DB 3; Length 20;
Best Local Similarity 93.8%; Pred. No. 76;
Matches 15: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 GGCCATCAGTCTCTG 19
DB 2 GGCCATCAGTCTCTG 17

RESULT 7

US-09-233-506-11/c
Sequence 11, Application US/09233506
Patent No. 6136580

GENERAL INFORMATION:

APPLICANT: Fukuda, Minoru
TITLE OF INVENTION: A Beta-1-6-N-Acetylglucosaminyltransferase That Forms
FILE REFERENCE: P-LJ 3415
CURRENT APPLICATION NUMBER: US/09/233,506
CURRENT FILING DATE: 1999-01-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 33
TYPE: DNA
ORGANISM: Homo sapiens
US-09-233-506-11

Query Match 69.5%; Score 13.2; DB 3; Length 33;
Best Local Similarity 83.3%; Pred. No. 3,4e+02;
Matches 15: Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CTGGGCATCAGTCTCTG 18
DB 24 CTGGGCATCAGTCTCTG 7

RESULT 8

US-08-584-040-4815/c
Sequence 4815, Application US/08584040
Patent No. 6346398

GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwigen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-6000
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4815:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: The letter "N" represents the stem II region
US-08-584-040-4815
Query Match 68.4%; Score 13; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 4,1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 7 CATGAGTCGCTG 19
DB 14 CATGAGTCGCTG 2
RESULT 9
US-09-182-728A-4/c
Sequence 4, Application US/09182728A
Patent No. 6238883
GENERAL INFORMATION:
APPLICANT: BROWN, ANTHONY
APPLICANT: CHAPMAN, CONRAD GERALD
APPLICANT: GLOGER, ISRAEL SIMON
APPLICANT: EVANS, JOANNE RACHEL
APPLICANT: CAIRNS, WILLIAM
APPLICANT: HERDON, HUGH
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30176

CURRENT APPLICATION NUMBER: US/09/182,728A
CURRENT FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 9818890.7
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 25
TYPE: DNA
ORGANISM: HOMO SAPIENS
US-09-182-728A-4
Query Match 67.4%; Score 12.8; DB 4; Length 25;
Best Local Similarity 87.5%; Pred. No. 5,2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 CTGGGCACTCAGTCT 16
DB 21 CTGGGCACTCAGTCT 6
RESULT 10
US-09-795-232-4/c
Sequence 4, Application US/09795232
Patent No. 6426405
GENERAL INFORMATION:
APPLICANT: Anthony M. Brown
APPLICANT: Conrad Gerald Chapman
APPLICANT: Israel Simon Gloger
APPLICANT: Joanne Rachel Evans
APPLICANT: William Cairns
APPLICANT: Hugh Jonathan Herdon
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30176-D1
CURRENT APPLICATION NUMBER: US/09/795,232
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 09/182,728
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 9818890.7
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 25
TYPE: DNA
ORGANISM: HOMO SAPIENS
US-09-795-232-4
Query Match 67.4%; Score 12.8; DB 4; Length 25;
Best Local Similarity 87.5%; Pred. No. 5,2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 CTGGGCACTCAGTCT 16
DB 21 CTGGGCACTCAGTCT 6
RESULT 11
US-08-960-190A-2
Sequence 2, Application US/08960190A
Patent No. 6232445
GENERAL INFORMATION:
APPLICANT: Rhode, Peter R.
APPLICANT: Acevedo, Jorge
APPLICANT: Burkhardt, Martin
APPLICANT: Jiao, Jin-an
APPLICANT: Wong, Hing C.
TITLE OF INVENTION: SOLUBLE HMC COMPLEXES AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dikey, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067,615
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/596,387
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/382,454
FILING DATE: 01-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,302
FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Pearson, Louise S.
REGISTRATION NUMBER: 32,369
REFERENCE/DOCKET NUMBER: STR-4665-CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 267-5300
TELEFAX: (708) 267-5376
INFORMATION FOR SEQ ID NO.: 40:
SEQUENCE CHARACTERISTICS:

PT Preventing asthma, allergies, hypereosinophilia, inflammation or cancer
PT
XX
PS Claim 5; Page 32; 72pp; English.
XX
CC This is an antisense oligonucleotide directed against the CCR3 receptor.
CC The antisense oligonucleotide inhibits CCR3 receptor expression. The CCR3
CC receptor is important in the recruitment of eosinophils into the sites of
CC allergic or asthmatic inflammation. The chemokines Eotaxin, MCP-4 and
CC RANTES mediate most of their effects through the CCR3 receptor. The
CC invention relates to antisense oligonucleotides directed against a
CC nucleic acid sequence encoding either a CCR3 receptor, a common subunit
CC of Interleukin-4 (IL-4) and Interleukin-13 (IL-13) receptors, or a common
CC subunit of IL-3, IL-5 and GM-CSF receptors. The antisense
CC oligonucleotides can be used in the treatment or prevention of asthma,
CC allergy, hypereosinophilia, general inflammation or cancer.
XX
SQ Sequence 19 BP; 2 A; 6 C; 6 G; 5 T; 0 other:

Query Match 100.0%; Score 19; DB 21; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTGCCTCTG 19
DB 1 CTGGCCATCAGTGCCTCTG 19

RESULT 2
AAQ95044/G
ID AAQ95044 standard; DNA: 45 BP.
XX
AC AAQ95044;
XX
DT 06-MAR-1996 (first entry)
XX
DE Human hippocampal neuropeptide Y2 receptor (-) strand DNA probe TM4.
XX
KW Hippocampus; brain; neuropeptide; peptide; hypertension; pain;
KW gastrointestinal disorder; diagnosis; sleeping disorder; epilepsy;
KW memory loss; diarrhoea; nasal congestion; DNA probe;
KW oligonucleotide; ss.
XX
OS Synthetic.
XX
PN W09521245-A1.
XX
PD 10-AUG-1995.
XX
PF 03-FEB-1995; 95MO-US01469.
XX
PR 03-FEB-1994; 94US-0192288.
XX
PA (SYNA-) SYNAPTIC PHARM CORP.
XX
PI Branchek T, Gerald C, Walker MW, Weinschank R;
XX
DR WPI: 1995-283765/37.
XX
PT Human and rat Y2 receptor DNA and protein - useful in diagnosis and
PT treatment of e.g. cognitive and gastrointestinal disorder(s),
PT hypertension and pain
XX
PS Disclosure: Page 50; 193pp; English.
XX
CC This oligonucleotide probe corresponding to nucleotides 531-600 of
CC human neuropeptide Y2 receptor cDNA and to a transmembrane region
CC of the amino acid sequence of the receptor, was used to obtain the
CC rat homologue of the human Y2 receptor.
XX
SQ Sequence 45 BP; 10 A; 13 C; 17 G; 5 T; 0 other;

Query Match 83.2%; Score 15.8; DB 16; Length 45;

Best Local Similarity 89.5%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTGCCTCTG 19
DB 43 CTGGCCATCAGTGCCTCTG 25

RESULT 3
AAQ95043
ID AAQ95043 standard; DNA: 45 BP.
XX
AC AAQ95043;
XX
DT 06-MAR-1996 (first entry)
XX
DE Human hippocampal neuropeptide Y2 receptor (+) strand DNA probe TM4.
XX
KW Hippocampus; brain; neuropeptide; peptide; hypertension; pain;
KW gastrointestinal disorder; diagnosis; sleeping disorder; epilepsy;
KW memory loss; diarrhoea; nasal congestion; DNA probe;
KW oligonucleotide; ss.
XX
OS Synthetic.
XX
PN W09521245-A1.
XX
PD 10-AUG-1995.
XX
PF 03-FEB-1995; 95MO-US01469.
XX
PR 03-FEB-1994; 94US-0192288.
XX
PA (SYNA-) SYNAPTIC PHARM CORP.
XX
PI Branchek T, Gerald C, Walker MW, Weinschank R;
XX
DR WPI: 1995-283765/37.
XX
PT Human and rat Y2 receptor DNA and protein - useful in diagnosis and
PT treatment of e.g. cognitive and gastrointestinal disorder(s),
PT hypertension and pain
XX
PS Disclosure: Page 50; 193pp; English.
XX
CC This oligonucleotide probe corresponding to nucleotides 531-600 of
CC human neuropeptide Y2 receptor cDNA and to a transmembrane region
CC of the amino acid sequence of the receptor, was used to obtain the
CC rat homologue of the human Y2 receptor.
XX
SQ Sequence 45 BP; 7 A; 12 C; 12 G; 14 T; 0 other;

Query Match 77.9%; Score 14.8; DB 16; Length 45;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTGCCTCT 18
DB 28 CTGGCCATCAGTGCCTCT 45

RESULT 4
AAV43277
ID AAV43277 standard; DNA: 20 BP.
XX
AC AAV43277;
XX
DT 26-OCT-1998 (first entry)
XX
DE primer JB586 for amplification-based detection of fungal ITS regions.
XX Internal transcribed spacer; ITS; detection; maize; fungal; pathogen;
KW PCR primer; ss.

XX OS Synthetic.
 XX OS Helminthosporium turcicum.
 XX PN EP859061-A2.
 XX PD 19-AUG-1998.
 XX PF 03-NOV-1997; 97EP-0810779.
 XX PR 01-NOV-1996; 96US-0742023.
 XX PA (NOVS) NOVARTIS AG.
 XX PI Beck JT.
 XX DR WPI: 1998-429687/37.
 XX PT New internal transcribed spacer sequences of maize fungal pathogens
 XX PT and primers and primer pairs - used to detect pathogens e.g.
 XX PT Helminthosporium carbonum, Cercospora zeae-maydis and Kabatiella
 XX PT zeae
 XX PS Claim 4; Page 11; 49pp; English.
 XX CC PCR primers AAV43277-303 are used to in amplification-based detection of
 XX CC maize fungal internal transcribed spacer (ITS) regions. They are used
 XX CC to identify Helminthosporium turcicum, H. maydis, H. carbonum,
 XX CC Kabatiella zeae and Cercospora zeae-maydis. The method comprises
 XX CC isolating DNA from a plant leaf infected with a pathogen, subjecting the
 XX CC DNA to PCR amplification using at least one primer derived from the ITS
 XX CC sequence.
 XX SQ Sequence 20 BP; 3 A; 5 C; 6 G; 6 T; 0 other;
 OY Query Match 75.8%; Score 14.4; DB 19; Length 20;
 Best Local Similarity 93.8%; Pred. No. 5.9e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 4 GGCCATCAGTCTCTG 19
 ||| |||||
 2 GGCCATCAGTCTCTG 17
 RESULT 5
 AAX97497
 ID AAX97497 standard; DNA: 20 BP.
 XX AC AAX97497;
 XX DT 13-SEP-1999 (first entry)
 XX DE Primer used to amplify Chlamydia pneumoniae polynucleotides.
 XX KM Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 XX KM sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
 XX KW vaccine; neutralising epitope; PCR primer; ss.
 XX OS Synthetic.
 XX OS Chlamydia pneumoniae.
 XX PN M09927105-A2.
 XX PD 03-JUN-1999.
 XX PF 20-NOV-1998; 98MO-IB01890.
 XX PR 04-NOV-1998; 98US-0107078.
 XX PR 21-NOV-1997; 97FR-0014673.
 XX PA (GEST) GENSET.
 XX PI Griffiths R;

XX XX WPI: 1999-357842/30.
 XX DR
 XX PT Genome sequence of Chlamydia pneumoniae
 XX PT
 XX PS Page 1909; Disclosure: 1912pp; English.
 XX CC AAX1991-X97517 represent PCR primers used to amplify open reading
 XX CC frames and other nucleic acid sequences from the genome of
 XX CC Chlamydia pneumoniae (see AAX9190). C. pneumoniae causes respiratory
 XX CC disease such as pneumonia and bronchitis and is thought to be a
 XX CC contributing factor in heart disease, sarcoidosis, sinusitis, purulent
 XX CC otitis media, erythema nodosum or pharyngitis. The polypeptides encoded
 XX CC by the open reading frames of the C. pneumoniae genome (see AAY34584-
 XX CC AAY35879) can be used in immunogenic compositions as vaccines. Vectors
 XX CC containing C. pneumoniae nucleotide sequences can also be used as
 XX CC immunogenic compositions, especially where the vector directs the
 XX CC expression of a neutralising epitope of C. pneumoniae.
 XX SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 other;
 OY Query Match 74.7%; Score 14.2; DB 20; Length 20;
 Best Local Similarity 84.2%; Pred. No. 7.5e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 DB 1 CTGGGCATCAGTCTCTG 19
 ||||| ||||| |||||
 1 CTGGCCATPAAGTACTCTG 19
 RESULT 6
 AAH41073/C
 ID AAH41073 standard; DNA: 36 BP.
 XX AC AAH41073;
 XX DT 03-SEP-2001 (first entry)
 XX DE PCR primer specific for ecdysone C-terminus insertion site DNA SEQ ID 29.
 XX KM Steroid hormone; thyroid hormone; receptor; DNA binding; PCR primer;
 XX KW chimeric protein; expression modulation; ecdysone receptor; ss.
 XX OS Unidentified.
 XX PN W0200136447-A2.
 XX PD 25-MAY-2001.
 XX PF 17-OCT-2000; 2000MO-US41224.
 XX PR 20-OCT-1999; 99US-0421971.
 XX PA (SALK) SALK INST BIOLOGICAL STUDIES.
 XX PI Gage FH, Suhrt ST, Gill EB, Senut MC;
 XX DR WPI: 2001-355608/37.
 XX DR
 XX PT Novel chimeric protein useful for modulating exogenous gene expression
 XX PT in subjects, comprises two functional protein units, each containing
 XX PT dimerization domain of steroid/thyroid hormone nuclear receptor
 XX PT superfamily -
 XX PS Example 1; Page 39; 60pp; English.
 XX CC The present invention relates to a chimeric protein which consists of at
 XX CC least two functional protein units where each protein unit comprises the
 XX CC dimerisation domain of a member of the steroid/thyroid hormone nuclear
 XX CC receptor superfamily. The protein units are linked by a linker peptide,
 XX CC and the two protein units form a functional entity. The invention
 XX CC includes a method for modulating the expression of an exogenous gene in
 XX CC an organism or cell containing the chimeric protein. The cell or organism

CC also contains a DNA construct comprising the exogenous gene under the control of a response element with which the chimeric protein interacts. The response element controls the expression of the exogenous gene. The method also involves administering to the subject or cell an effective amount of an exogenous ligand for at least one functional unit of the chimeric protein. The chimeric protein is useful for modulating the expression of an exogenous gene in a subject organism. The present sequence represents a PCR primer specific for DNA encoding the C-terminus insertion site of the ecdysone receptor. The PCR product is used in an example illustrating the construction of a chimeric protein of the invention.

Sequence 36 BP; 6 A; 9 C; 12 G; 9 T; 0 other;

Query Match 74.7%; Score 14.2; DB 22; Length 36;

Best Local Similarity 84.2%; Pred. No. 8.1e+02; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CTGGCCATCAGTCTCTG 19
| | | | | | | | | | | | | | | | | | | | | |
Db 27 CTGGCCACAGCCCTCTG 9

RESULT 7

AA66407/c
ID AA66407 standard; DNA: 47 BP.

AA66407;

10-SEP-2001 (first entry)

Human map-related biallelic marker seq ID NO:754.

XX Human genome: biallelic marker; high density disequilibrium map;
XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX haplotyping; hybridisation; identification; characterisation;
XX diagnosis; single nucleotide polymorphism; SNP; ds.

OS Homo sapiens.

XX Key Location/Qualifiers
XX replace(24,C)
XX /tag= a
XX /standard_name= "single nucleotide polymorphism"

W0954500-A2.

28-OCT-1999.

21-APR-1999; 99WC-IB00822.

21-APR-1998; 98US-0082614.

23-NOV-1998; 98US-0109732.

(G8ST) GENSET.

Cohen D, Blumenfeld M, Chumakov I;

WPI: 2000-013267/01.

Claim 1: Page 391; 2745pp; English.

CC AA665654 to AA665678 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AA665679 to AA677440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also

CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.

Sequence 47 BP; 12 A; 17 C; 8 G; 10 T; 0 other;

Query Match 70.5%; Score 13.4; DB 21; Length 47;

Best Local Similarity 93.3%; Pred. No. 2.2e+03; Mismatches 1; Indels 0; Gaps 0;

Oy 3 GGGCCATCAGTCTCTG 17
| | | | | | | | | | | | | | | | | | | | | |
Db 34 GGGCCATCAGTCTCTG 20

RESULT 8

AA62140/c
ID AAC62140 standard; DNA: 33 BP.

AA62140;

06-MAR-2001 (first entry)

PCR primer for beta-1-6-N-acetylglucosaminyltransferase DNA fragment.

XX Human: beta-1-6-N-acetylglucosaminyltransferase; C2GNT-M; Inflammation;
XX membrane protein; branched steryl lex; L-selectin; immune reaction;
XX inflammation; tissue rejection; tumour metastasis; PCR primer: ss.

OS Mus musculus.

PN US6136580-A.

24-OCT-2000.

19-JAN-1999; 99US-0233506.

19-JAN-1999; 99US-0233506.

(BURN-) BURNHAM INST.

Fukuda M, Yeh J;

WPI: 2001-040238/05.

CC New C2GNT-M polypeptides having core 2, core 4 and I branching
CC beta-1-6-N-acetylglucosaminyltransferase activities for preparing
CC reagents useful for diagnosing, preventing or treating inflammation or
CC tumour metastasis
CC Example 5: Column 21; 25pp; English.

CC PCR primers AAC62140-41 were used to amplify a DNA fragment encoding a
CC beta-1-6-N-acetylglucosaminyltransferase polypeptide, with core2, core4
CC and I branching activities. It is designated C2GNT-M. C2GNT-M is a
CC membrane protein that is predominantly expressed in colon, small
CC intestine, trachea, stomach and thyroid, as well as in certain cancer
CC cell lines. C2GNT-M polypeptides may be used to prepare molecules having
CC highly branched steryl lex and L-selectins, which may be subsequently
CC used to modulate immune reactions, e.g. inflammation and tissue
CC rejection, and to prevent or inhibit tumour metastasis.

Sequence 33 BP; 8 A; 8 C; 10 G; 7 T; 0 other;

Query Match 69.5%; Score 13.2; DB 22; Length 33;

Best Local Similarity 83.3%; Pred. No. 2.6e+03; Mismatches 3; Indels 0; Gaps 0;

QY	1	CTGGCCATCAGTCTCT	18
DB	24	CTGACATCTCTCTCT	7
XX	AAZ65460	standard; DNA; 47 BP.	
XX	AAZ65460:		
XX	10-SEP-2001	(first entry)	
XX	Human map-related	biallelic marker SEQ ID NO:807.	
XX	Human genome;	biallelic marker; high density disequilibrium map;	
XX	genomic map;	haplotype; phenotype; polymorphic base; genotyping;	
XX	haplotyping;	hybridisation; identification; characterisation;	
XX	diagnosis;	single nucleotide polymorphism; SNP; ds.	
XX	Homo sapiens.		
XX	Key	Location/Qualifiers	
XX	variation	replace(24.C)	
XX		/*tag= a	
XX		/standard_name="single nucleotide polymorphism"	
XX	W09954500-A2.		
XX	28-OCT-1999.		
XX	21-APR-1999;	99W0-IB00822.	
XX	21-APR-1998;	98US-0082614.	
XX	23-NOV-1998;	98US-0109732.	
XX	(GEST)	GENSET.	
XX	Cohen D, Blumenfeld M, Chumakov I;		
XX	WPI: 2000-013267/01.		
XX	Novel biallelic markers	used to construct a high density disequilibrium	
XX	map of the human genome		
XX	Claim 1;	Page 402; 2745pp; English.	
XX	AAZ65654	to AAZ659578 represent human biallelic markers from the present	
XX	invention,	which contain a polymorphic base at position 24 of their	
XX	nucleotide sequences.	AAZ659579 to AAZ77440 represent amplification	
XX	primers for the biallelic markers.	The biallelic markers of the	
XX	invention have a variety of uses:	they can be used for high density	
XX	mapping of the human genome,	and in complex association studies and	
XX	haplotyping studies	which are useful in determining the genetic basis	
XX	for disease states.	Compositions and methods of the invention can also	
XX	be useful for the identification	of the targets for the development of	
XX	pharmaceutical agents	and diagnostic methods, as well as the	
XX	characterisation of the differential	efficacious responses to and side	
XX	effects from pharmaceutical agents	acting on a disease as well as other	
XX	treatment.		
XX	N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297		
XX	and 3367, are not actually given a sequence in the Sequence Listing		
XX	from the present invention.		
XX	Sequence 47 BP; 10 A; 12 C; 15 G; 10 T; 0 other;		
QY	Query Match	69.5%; Score 13.2; DB 21; Length 47;	
QY	Best Local Similarity	83.3%; Pred. NO. 2.7e+03;	
QY	Matches 15; Conservative	0; Mismatches 3; Indels 0; Gaps 0;	
DB	2	TGGGCCATCAGTCTCTG 19	
DB	15	TGGGCCCTTGAGAGCTCTG 32	

RESULT 10
 AAH38907/C
 ID AAH38907 standard; DNA: 25 BP.
 XX
 AC AAH38907:
 XX
 DT 14-Aug-2001 (first entry)
 XX
 DE SNP specific SNPE primer SEQ ID 1703.
 XX
 Single nucleotide polymorphism: SNP: single nucleotide primer extension;
 KM SNE: genotyping; agammaglobulinemia; diabetes insipidus; cancer;
 KM Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;
 KM polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
 KM acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
 KM inflammation; forensic investigation; paternity analysis; primer: ss.
 OS Homo sapiens.
 XX
 PN W0200129262-A2.
 PD 26-Apr-2001.
 XX
 PF 13-Oct-2000; 2000MO-US28436.
 XX
 PR 15-Oct-1999; 9905-0160096.
 XX
 PA (ORCH-) ORCHID BIOSCIENCES INC.
 PI Picoult-Newburg L., Pohl M;
 DR WPI: 2001-290930/30.
 XX
 PT New genotyping oligonucleotide, useful for detecting the presence,
 XX absence or identity of single polynucleotide polymorphism in a nucleic
 PT acid sample.
 XX
 Claim 1; Page 58; 83pp; English.
 PS
 XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
 CC primer extension (SNPE) primers, and the sequences of regions flanking
 CC sites of single nucleotide polymorphisms SNPs. The present invention
 CC includes kits for determining the presence or absence of a SNP, using the
 CC oligonucleotides of the invention. The PCR primers are used to amplify a
 CC SNP flanking sequence, the SNP primer is used as a genotyping primer.
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by
 CC performing a single-nucleotide primer extension reaction. The
 CC oligonucleotides are useful for determining the presence, absence or
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
 CC assess by association analysis the genotype of an individual or group of
 CC individuals, having a pathological phenotypic trait suspected of being
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
 CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
 CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
 CC traits also include symptoms of or susceptibility to multifactorial
 CC disease of which a component is or may be genetic such as autoimmune
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,
 CC inflammation, cancer, nervous system diseases and infection by pathogenic
 CC microorganism. The method is also useful in forensic investigations and
 CC paternity analysis. The present sequence represents a single nucleotide
 CC primer extension (SNPE) primer specific for a human SNP containing DNA
 CC sequence.
 XX
 Sequence 25 BP; 4 A; 4 C; 10 G; 6 T; 1 other;
 Query Match 68.4%; Score 13; DB 22; Length 25;
 Best Local Similarity 86.7%; Pred. No. 3.2e+03;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 5 GCATGACGCTCTG 19
 GCATGACGCTCTG 19

```

|||||
DB      19  CCCTCAGACTCTG  5

RESULT 11
AAZ72065/c
ID      AAZ72065 standard; RNA: 27 BP.
XX
AC      AAZ72065;
XX
DT      28-JUL-1999 (first entry)
XX
DE      Mouse fli-1 VEGF receptor hammerhead ribozyme #309.
XX
KW      Vascular endothelial growth factor receptor; VEGF receptor; fli-1;
KW      fli-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW      tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW      fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW      foetal liver kinase 1; ss.
XX
OS      Synthetic.
OS      Mus sp.
XX
PN      M09715662-A2.
XX
PD      01-MAY-1997.
XX
PF      25-OCT-1996; 96MO-US17480.
XX
PR      11-JAN-1996; 96US-0584040.
PR      26-OCT-1995; 95US-0005974.
XX
PA      (CHIR ) CHIRON CORP.
PA      (RIBO-) RIBOZYME PHARM INC.
XX
PI      Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
XX
DR      WPI: 1997-259017/23.
XX
PT      Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT      mRNA stability - useful for treating e.g. tumour angiogenesis,
PT      psoriasis, rheumatoid arthritis, etc., in a human patient
XX
PS      Claim 9; Page 132; 218pp; English.
XX
CC      The present invention describes nucleic acid molecules which modulate
CC      the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC      receptors of vascular endothelial growth factor (VEGF). A patient
CC      (preferably human) having a condition associated with the level of the
CC      fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC      receptor (KDR) and/or foetal liver kinase 1 (Flk-1) (e.g. tumour
CC      angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC      be treated by administering the nucleic acid molecule or the expression
CC      vector to the patient. AAX67275 to AAX75752 represent specific examples
CC      of nucleic acid molecules from the present invention.
XX
SQ      Sequence 27 BP; 10 A; 5 C; 7 G; 4 U; 1 other;
XX
Query Match      68.4%; Score 13; DB 18; Length 27;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      7 CATCAGTGTCTG 19
DB      14 CATCAGTGTCTG 2
XX
RESULT 12
AAZ62041/c
ID      AAZ62041 standard; RNA: 27 BP.
XX
AC      AAZ62041;
XX

```

```

DT      28-MAR-2000 (first entry)
XX
DE      Hammerhead ribozyme HCV-2704 cleaves HCV RNA at nt. Position 2704.
XX
KW      Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW      cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW      autoimmune disease; ss.
XX
OS      Synthetic.
XX
FH      Key Location/Qualifiers
FH      misc_difference 16
FH      /tag= a
FH      /note= "hammerhead ribozyme stem-loop II (as defined
FT      by Hettel et al., NAR 20:3252 (1992))."
XX
XX      M09955847-A2.
XX
XX      04-NOV-1999.
XX
XX      26-APR-1999; 99WO-US09027.
XX
XX      27-APR-1998; 98US-0083217.
XX      18-SEP-1998; 98US-0100842.
XX      25-FEB-1999; 99US-0257608.
XX      23-MAR-1999; 99US-0274553.
XX
XX      (RIBO-) RIBOZYME PHARM INC.
XX
XX      Blatt L, McSwiggen JA, Roberts E, Pavco PA, Macejak D;
XX
XX      WPI: 2000-062023/05.
XX
XX      Novel ribozymes for the treatment of diseases and conditions related to
XX      hepatitis C infection -
XX
XX      Claim 8; Page 55; 123pp; English.
XX
XX      The present sequence represents an enzymatic nucleic acid, especially
XX      a hammerhead ribozyme, which cleaves the hepatitis C virus (HCV) RNA
XX      sequence at the base position indicated in the descriptor line.
XX      The HCV sequence was screened for optimal ribozyme target sites using
XX      a computer folding algorithm and regions of the mRNA which did not form
XX      secondary folding structures and contained potential ribozyme cleavage
XX      sites were identified. Ribozymes were synthesised to target these sites
XX      and their activities optimised by either varying the length of the
XX      binding arms or by modification to prevent degradation by nucleases.
XX      The ribozymes of the invention inhibit gene expression and/or viral
XX      replication, and are used to treat diseases associated with hepatitis C
XX      virus (HCV) infection, e.g. cirrhosis, liver failure and hepatocellular
XX      carcinoma. The ribozymes may be used in combination with interferon to
XX      treat HCV infection, other infectious diseases, autoimmune diseases, and
XX      cancer.
XX
SQ      Sequence 27 BP; 8 A; 7 C; 8 G; 3 U; 1 other;
XX
Query Match      68.4%; Score 13; DB 21; Length 27;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      7 CATCAGTGTCTG 19
DB      13 CATCAGTGTCTG 1
XX
RESULT 13
AAF06658/c
ID      AAF06658 standard; RNA: 29 BP.
XX
AC      AAF06658;
XX
DT      16-FEB-2001 (first entry)
XX

```

DE Hammerhead ribozyme #3455.
 XX
 KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KM Interferon alpha; ss.
 XX
 OS Homo sapiens.
 PN W0200061729-A2.
 PD 19-OCT-2000.
 PF 11-APR-2000; 2000WO-US09721.
 PR 12-APR-1999; 99US-0129390.
 PA (RIBO-) RIBOZYME PHARM INC.
 PI Blatt L, Zwick M, Pavco P, McSwiggen J;
 DR WPI; 2000-647423/62.
 XX
 PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor
 PT protein, interferon alpha and erythropoietin .
 PS
 PS Claim 59; Page 135; 164pp; English.
 CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EARI/COUP-TF1, the GATA
 CC transcription factor gene, IRF-2 and/or the C/EBP displacement
 CC protein (CDP). Inhibition of the repressors removes prevents
 CC inhibition (and consequently increases expression of) genes involved in
 CC the production of erythropoietin, granulocyte colony stimulating factor
 CC protein and interferon alpha .
 XX
 SQ Sequence 29 BP; 9 A; 7 C; 10 G; 2 U; 1 other:
 Query Match 68.4%; Score 13; DB 21; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 YY 7 CATCAGTGCCTCTG 19
 DB 14 CATCAGTGCCTCTG 2

RESULT 14
 AAA24583/c
 ID AAA24583 standard; RNA; 29 BP.
 AC AAA24583;
 XX
 DT 19-JUL-2000 (first entry)
 DE Oestrogen receptor hammerhead ribozyme sequence SEQ ID NO:1081.
 KW Oestrogen receptor; c-rta; k-ras; bcl-2; ribozyme; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KW gene expression modification; cancer; phosphorothioate; endonuclease;
 KW anticancer; breast cancer; endometrium cancer; ss.
 XX
 OS Homo sapiens.
 PN W09954459-A2.
 PD 28-OCT-1999.
 PF 19-APR-1999; 99WO-US08547.
 PR 20-APR-1998; 98US-0082404.
 PR 23-JUN-1998; 98US-0103636.
 XX

PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Thompson JD, Beigelman L, McSwiggen JA, Karpelsky A, Bellon L;
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haederil P;
 PI Matulic-Adamic J;
 XX
 DR WPI; 2000-013248/01.
 PT
 PT New nucleic acids that interact, and optionally cleave, target
 PT sequences, used to treat cancer .
 PS
 PS Claim 51; Page 91; 148pp; English.
 CC
 CC The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphorodithioate
 CC link, having endonuclease activity. (A), and more generally any
 CC catalytic nucleic acid (A') that modulates expression of the estrogen
 CC receptor gene, are used to treat cancer (particularly of breast or
 CC endometrium), in vivo or by transforming cells ex vivo and implanting
 CC treated cells, or for other conditions associated with levels of
 CC estrogen receptor. Because of the high selectivity for targeted
 CC can also be used to correlate inhibition of gene expression with
 CC alterations in phenotype, particularly for identification of therapeutic
 CC targets, and as research reagents (for RNA, in the same way that
 CC restriction endonucleases are used with DNA). The combination of
 CC modifications in (A) improves resistance to nucleases, binding affinity
 CC and/or activity. AAA23503 to AAA24747 represent estrogen receptor
 CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
 CC corresponding target sequences. AAA25993 to AAA26105 represent estrogen
 CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
 CC their corresponding target sequences. AAA26219 to AAA26271 represent
 CC other ribozyme sequences and antisense oligonucleotides used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 29 BP; 12 A; 5 C; 7 G; 4 U; 1 other:
 Query Match 68.4%; Score 13; DB 21; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 YY 7 CATCAGTGCCTCTG 19
 DB 14 CATCAGTGCCTCTG 2

RESULT 15
 ABN06590/c
 ID ABN06590 standard; DNA; 17 BP.
 AC ABN06590;
 XX
 DT 29-MAY-2002 (first entry)
 DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6582.
 KW Human; genome-derived myosin-like protein 1; GDMLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 PN W0200192524-A2.
 PD 06-DEC-2001.
 PF 25-MAY-2001; 2001WO-US16981.
 PR 26-MAY-2000; 2000US-207456P.
 PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024283.
 PR 30-JAN-2001; 2001WO-US00661.
 PR 30-JAN-2001; 2001WO-US00662.
 XX

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OM nucleic - nucleic search, using sw model

Run on: November 28, 2002, 16:42:34 ; Search time 1103.97 Seconds

(without alignments)
500.879 Million cell updates/sec

Title: US-09-719-737-18
Perfect score: 18

Perfect score: 19

Sequence: 1 ctgggcattcagtgctctg 19

Scoring table: IDENTITY_NUC

Gapor 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database

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18:  17:  em_hum.*
19:  18:  em_in.*
20:  19:  em_mu.*
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23:  22:  em_pat.*
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25:  24:  em_pl.*
26:  25:  em_r.*
27:  26:  em_scs.*
28:  27:  em_un.*
29:  28:  em_v1.*
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39:  38:  em_hngo_hum.*
40:  39:  em_hngo_mus.*
41:  40:  em_hngo_other.*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	19	100.0	19	6	AX008665	AX008665 Sequence
C 2	19	100.0	19	6	AX008666	AX008666 Sequence
C 3	15.8	83.2	45	6	AR088040	AR088040 Sequence
4	14.8	77.9	45	6	AR088049	AR088049 Sequence
5	14.4	75.8	20	6	AR036920	AR036920 Sequence
6	14.4	75.8	20	6	AR092725	AR092725 Sequence
C 7	13.2	69.5	33	6	AR136084	AR136084 Sequence
8	13.2	69.5	40	6	I05997	I05997 Sequence
9	13.2	69.5	44	6	I08796	I08796 Sequence
C 10	13	68.4	25	6	AX116580	AX116580 Sequence
C 11	13	68.4	27	6	AR189327	AR189327 Sequence
C 12	12.8	67.4	25	6	AR154271	AR154271 Sequence
C 13	12.8	67.4	25	6	E38405	E38405 SC6 polypep
14	12.6	66.3	19	6	AX115503	AX115503 Sequence
15	12.6	66.3	43	6	AR152008	AR152008 Sequence
16	12.6	66.3	44	6	AR033897	AR033897 Sequence
17	12.6	66.3	44	6	AR175030	AR175030 Sequence
18	12.0	66.3	44	6	AX032462	AX032462 Sequence
19	12.0	66.3	44	6	E15948	E15948 Primer: 7/1
20	12.6	66.3	50	6	AX164813	AX164813 Sequence
C 21	12.4	65.3	18	6	A76055	A76055 Sequence
C 22	12.4	65.3	21	6	AX095087	AX095087 Sequence
23	12.4	65.3	31	6	AR090047	AR090047 Sequence
24	12.4	65.3	31	6	AR197082	AR197082 Sequence
25	12.4	65.3	31	6	I37209	I37209 Sequence
26	12.4	65.3	31	6	I37210	I37210 Sequence
27	12.4	65.3	31	6	I37211	I37211 Sequence
28	12.4	65.3	31	6	I94059	I94059 Sequence
29	12.4	65.3	31	6	I94060	I94060 Sequence
30	12.4	65.3	31	6	I94061	I94061 Sequence
31	12.4	65.3	40	6	A59027	A59027 Sequence
32	12.4	65.3	40	6	AR195544	AR195544 Sequence
33	12.4	65.3	45	6	HSBRT1160	HSBRT1160 Sequence
C 34	12.2	64.2	20	6	AX418798	AX418798 Sequence
C 35	12.2	64.2	21	6	A25404	A25404 CE gene mut
36	12.2	64.2	21	6	A25412	A25412 CE gene mut
C 37	12.2	64.2	31	6	AX424921	AX424921 Sequence
C 38	12.2	64.2	35	6	E36412	E36412 Protein rel
C 39	12.2	64.2	36	6	E16104	E16104 PCR primer
C 40	12.2	64.2	40	6	AX092544	AX092544 Sequence
C 41	12.2	64.2	45	6	AR032344	AR032344 Sequence
C 42	12.2	64.2	50	6	AX157400	AX157400 Sequence
43	12	63.2	20	6	AR130810	AR130810 Sequence
44	12	63.2	21	6	AR103495	AR103495 Sequence
C 45	12	63.2	21	6	AX096839	AX096839 Sequence

ALIGNMENTS

RESULT 1	AX008665	LOCUS	AX008665	DEFINITION	Sequence 19	19 bp	DNA	Linear	PAT 06-SEP-2000
					from RefSeq: M000567.2				

ORGANISM	synthetic construct
REFERENCE	artificial sequences
1	(bases 1 to 19)

TITLE	Antisense oligonucleotides for treating or preventing atopic diseases and neoplastic cell proliferation
JOURNAL	Patent: WO 9966037-A 18 23-DEC-1999;

REMI PAOLO (CA): RECI EXPERTISES ET DEV MEDICAU (CA)

FEATURES
Location/Qualifiers
1. .19

/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Antisense oligonucleotide inhibiting the CCR3 human receptor"

BASE COUNT 2 a 6 c 6 g 5 t

ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.8;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCATCACTGCTCTG 19
|||||

Db 1 CTGGGCATCACTGCTCTG 19

RESULT 2
AX008666/c

LOCUS AX008666 19 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 19 from Patent WO9966037.

ACCESSION AX008666
VERSION AX008666.1 GI:9996190

KEYWORDS
SOURCE synthetic construct.

ORGANISM
synthetic construct
artificial sequences.

REFERENCE
AUTHORS
1 (bases 1 to 19)

TITLE
Antisense oligonucleotides for treating or preventing autistic diseases and neoplastic cell proliferation

JOURNAL
Patent: WO 9966037-A 19 23-DEC-1999;
REMI PAOLO (CA): RECI EXPERTISES ET DEV MEDICAU (CA)

FEATURES
Location/Qualifiers
1. .19

/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Sense oligonucleotide for the CCR3 human receptor"

BASE COUNT 5 a 6 c 6 g 2 t

ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.8;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCATCACTGCTCTG 19
|||||

Db 19 CTGGGCATCACTGCTCTG 1

RESULT 3
AR088050/c

LOCUS AR088050 45 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 14 from patent US 5989834.

ACCESSION AR088050
VERSION AR088050.1 GI:10014813

KEYWORDS
SOURCE Unknown.

ORGANISM
Unknown.
Unclassified.

REFERENCE
AUTHORS
1 (bases 1 to 45)
Gerald,C., Walker,M.W., Branchek,T. and Weinschenk,R.L.

TITLE
Uses of nucleic acid encoding neuropeptide Y/peptide YY (Y2) receptors nucleic acid encoding

JOURNAL
Patent: US 5989834-A 14 23-NOV-1999;
Location/Qualifiers
1. .45

BASE COUNT 10 a 13 c 17 g 5 t

ORIGIN

Query Match 83.2%; Score 15.8; DB 6; Length 45;
Best Local Similarity 89.5%; Pred. No. 5.7e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGGGCATCACTGCTCTG 19
|||||

Db 43 CTGGGCATCACTGCTCTG 25

RESULT 4
AR088049

LOCUS AR088049 45 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 13 from patent US 5989834.

ACCESSION AR088049
VERSION AR088049.1 GI:10014812

KEYWORDS
SOURCE Unknown.

ORGANISM
Unknown.
Unclassified.

REFERENCE
AUTHORS
1 (bases 1 to 45)
Gerald,C., Walker,M.W., Branchek,T. and Weinschenk,R.L.

TITLE
Uses of nucleic acid encoding neuropeptide Y/peptide YY (Y2) receptors nucleic acid encoding

JOURNAL
Patent: US 5989834-A 13 23-NOV-1999;
Location/Qualifiers
1. .45

BASE COUNT 7 a 12 c 12 g 14 t

ORIGIN

Query Match 77.9%; Score 14.8; DB 6; Length 45;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGGGCATCACTGCTCTG 18
|||||

Db 28 CTGGGCATCACTGCTCTG 45

RESULT 5
AR036920

LOCUS AR036920 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 15 from patent US 5800997.

ACCESSION AR036920
VERSION AR036920.1 GI:5954776

KEYWORDS
SOURCE Unknown.

ORGANISM
Unknown.
Unclassified.

REFERENCE
AUTHORS
1 (bases 1 to 20)
Beck,J.Joseph.

TITLE
Detection of maize fungal pathogens using the polymerase chain reaction

JOURNAL
Patent: US 5800997-A 15 01-SEP-1998;
Location/Qualifiers
1. .20

BASE COUNT 3 a 5 c 6 g 6 t

ORIGIN

Query Match 75.8%; Score 14.4; DB 6; Length 20;
Best Local Similarity 93.8%; Pred. No. 3.6e+03;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGCATCACTGCTCTG 19
|||||

Db 2 GGCATCACTGCTCTG 17

RESULT 6
AR097255

LOCUS AR097255 20 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 15 from patent US 6071698.


```

ACCESSION   AR097255
VERSION     AR097255.1  GI:12805985
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Beck,J,Joseph.
TITLE       DNA extraction buffer and method of use thereof
JOURNAL     Patent: US 6071698-A 15 06-JUN-2000;
FEATURES
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              /organism="unknown"
BASE COUNT   3 a      5 c      6 g
ORIGIN
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Best Local Similarity 93.8%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGGCATCAGTGTCTG 19
    ||| ||||| |||||
Db 2 GGCATCATGTCTCTG 17

RESULT 7
ARI36084/c  ARI36084 33 bp DNA linear PAT 16-JUN-2001
LOCUS      Sequence 11 from patent US 6136580.
ACCESSION  ARI36084
VERSION    ARI36084.1  GI:14476756
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 33)
AUTHORS     Fukuda,M. and Yeh,J.-C.
TITLE       beta.-1-6-N-acetylglucosaminyltransferase that forms core 2, core
            4 and 1 branches
JOURNAL     Patent: US 6136580-A 11 24-OCT-2000;
FEATURES
    source   1..33
              /organism="unknown"
BASE COUNT   8 a      8 c      10 g      7 t
ORIGIN
Query Match      69.5%; Score 13.2; DB 6; Length 33;
Best Local Similarity 83.3%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTGTCT 18
    |||| ||||| |||||
Db 24 CTGGACCATCTGTCT 7

RESULT 8
I05997      I05997 40 bp DNA linear PAT 02-DEC-1994
LOCUS      Sequence 14 from Patent EP 0275856.
ACCESSION  I05997
VERSION    I05997.1  GI:590816
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 40)
AUTHORS     Bollen,A.J., Gheysen,D., Jacobs,P., Pierard,L. and Collen,D.J.
TITLE       New plasmidogen activators
JOURNAL     Patent: EP 0275856-A1 14 27-JUL-1988;
FEATURES
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              /organism="unknown"
BASE COUNT   9 a      9 c      12 g      9 t      1 others

```

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ORIGIN
Query Match      69.5%; Score 13.2; DB 6; Length 40;
Best Local Similarity 83.3%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGGGCCATCAGTGTCTG 19
    ||| ||||| |||||
Db 19 TGTCCATCAGTGTCTG 36

RESULT 9
I08796      I08796 44 bp DNA linear PAT 02-DEC-1994
LOCUS      Sequence 18 from Patent WO 8804690.
ACCESSION  I08796
VERSION    I08796.1  GI:588501
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 44)
AUTHORS     Bollen,A.J., Gheysen,D., Jacobs,P., Pierard,L. and Collen,D.J.
JOURNAL     Patent: WO 8804690-A 18 30-JUN-1988;
FEATURES
    source   1..44
              /organism="unknown"
BASE COUNT  10 a     10 c     14 g     10 t
ORIGIN
Query Match      69.5%; Score 13.2; DB 6; Length 44;
Best Local Similarity 83.3%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGGGCCATCAGTGTCTG 19
    ||| ||||| |||||
Db 19 TGTCCATCAGTGTCTG 36

RESULT 10
AX116580/c  AX116580 25 bp DNA linear PAT 11-MAY-2001
LOCUS      Sequence 1703 from Patent WO0129262.
ACCESSION  AX116580
VERSION    AX116580.1  GI:14033522
KEYWORDS
SOURCE     synthetic construct.
ORGANISM   synthetic construct.
REFERENCE   1 (bases 1 to 25)
AUTHORS     Picoult-Newburg,L. and Pohl,M.
TITLE       Genotyping reagents, kits and methods of use thereof
JOURNAL     Patent: WO 0129262-A 1703 26-APR-2001;
FEATURES
    source   1..25
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="Primer"
BASE COUNT   4 a      4 c      10 g      6 t      1 others
ORIGIN
Query Match      68.4%; Score 13; DB 6; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.3e+04;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGCATCAGTGTCTG 19
    ||| ||||| |||||
Db 19 GGCATCAGTGTCTG 5

RESULT 11
ARI89327/c

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LOCUS AR189327 27 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 4815 from patent US 6346398.
ACCESSION AR189327
VERSION AR189327.1 GI:20235292
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 4815 12-FEB-2002;
FEATURES
source 1..27
BASE COUNT 10 a 5 c 7 g 4 t 1 others
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 CATGACGTCTCTG 19
Db 14 CATGACGTCTCTG 2
RESULT 12
AR154271/c AR154271 25 bp DNA linear PAT 08-AUG-2001
LOCUS AR154271
DEFINITION Sequence 4 from patent US 6238883.
ACCESSION AR154271
VERSION AR154271.1 GI:15122324
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Brown, A.M., Chapman, C.Gerald, Gloger, I., Simon, J., Evans, J., Rachel, J., Cairns, W. and Herdon, H. Jonathan.
TITLE Neurotransmitter transporter SC6
JOURNAL Patent: US 6238883-A 4 28-MAY-2001;
FEATURES
source 1..25
BASE COUNT 5 a 8 c 7 g 5 t
ORIGIN
Query Match 67.4% Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CTGGCCATCAGTCTCT 16
Db 21 CTGGCCACTCAGTCT 6
RESULT 13
E38405/c E38405 25 bp DNA linear PAT 31-JAN-2002
LOCUS E38405
DEFINITION SC6 polypeptide and SC6 polynucleotide.
ACCESSION E38405
VERSION E38405.1 GI:18624976
KEYWORDS JP 2000069981-A/3.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 25)
AUTHORS Brown, A.M., Chapman, K.J., Groga, I.S., Evans, J.R., Kern, W. and Haddon, H.
TITLE SC6 polypeptide and SC6 polynucleotide
JOURNAL Patent: JP 2000069981-A 3 07-MAR-2000;

COMMENT
SMITHKLINE BEECHAM CORP PUBLIC LTD CO
OS Artificial Sequence
PN JP 2000069981-A/3
PD 07-MAR-2000
PF 12-FEB-1999 JP 1999035070
PR 28-AUG-1998 GB 9818890.7
PI ANTHONY M BROWN, KONRAD JERROLD CHAPMAN, ISRAEL SIMON GROGA, PI
JOAN REYCHEL EVANS, WILLIAM KERN, HYU HADDON
PC C12N15/09,A61K31/00,A61K31/00,A61K31/00,A61K31/00,
PC A61K39/00,
PC A61K45/00,A61K48/00,C07K14/47,C07K14/705,C07K16/28,C12N5/10,
PC C12P21/02,
PC C12Q1/68,C01N33/53,C01N33/566,C01N33/577//C12P21/08,C12N15/00,
PC C12N5/00
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FH Key location/Qualifiers
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source 1..25
Location/Qualifiers
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/db_xref="taxon:32630"
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ORIGIN
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Best Local Similarity 87.5%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CTGGCCATCAGTCTCT 16
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RESULT 14
AX115503 AX115503 19 bp DNA linear PAT 11-MAY-2001
LOCUS AX115503
DEFINITION Sequence 626 from patent WO0129262.
ACCESSION AX115503
VERSION AX115503.1 GI:14032445
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 19)
AUTHORS Picoult-Newbury, L. and Pohl, M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 626 26-APR-2001;
FEATURES
source 1..19
Location/Qualifiers
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ORIGIN
Query Match 66.3% Score 12.6; DB 6; Length 19;
Best Local Similarity 78.9%; Pred. No. 3.9e+04;
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QY 1 CTGGCCATCAGTCTCTG 19
Db 1 CAGAGCCATCAGTCTCCG 19
RESULT 15
AR152008 AR152008 43 bp DNA linear PAT 08-AUG-2001
LOCUS AR152008
DEFINITION Sequence 2 from patent US 6232445.
ACCESSION AR152008
VERSION AR152008.1 GI:15118058
KEYWORDS

